

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

(without alignments)
15401.427 Million cell updates/sec

996

Sequence: 1 atgcagctaagtgtccctg.....tgaacttacagaccacgcc 966

Scoring table:

| IDENTITY_NUC | Percent 100 |
|--------------|-------------|
| 100 | 100 |

Searched: 2054640 seqs, 14551402878 residues

number of hits satisfying chosen parameters: 4109280

Maximum DB seq length: 20000000000

| | | |
|------------------|---------------|------|
| Post-processing: | Minimum Match | 0% |
| | Maximum Match | 100% |

Listing first 45 summarless

Database

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1:  gb_ba:*
2:  gb_htg:*
3:  gb_in:*
4:  gb_om:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
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35: em_htg_rod:*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 2 | 966 | 100.0 | 2718 | 6 | AA100591 | AA100591 Sequence |
| 3 | 966 | 100.0 | 2718 | 10 | AF199027 | AF199027 Mus muscu |
| 4 | 966 | 100.0 | 2803 | 10 | BC029227 | BC029227 Mus muscu |
| 5 | 956.8 | 99.0 | 1759 | 6 | AA100593 | AA100593 Sequence |
| 6 | 956.8 | 99.0 | 1759 | 10 | AF394451 | AF394451 Mus muscu |
| 7 | 360 | 37.3 | 158049 | 2 | AC015691 | AC015691 Mus muscu |
| 8 | 299.6 | 31.0 | 909 | 9 | AF216749 | AF216749 Homo sapl |
| 9 | 299.6 | 31.0 | 953 | 6 | AA100595 | AA100595 Sequence |
| 10 | 299.6 | 31.0 | 1009 | 9 | AF199028 | AF199028 Homo sapl |
| 11 | 299.6 | 31.0 | 1548 | 6 | AX083950 | AX083950 Sequence |
| 12 | 299.6 | 31.0 | 1572 | 9 | AF289028 | AF289028 Homo sapl |
| 13 | 299.6 | 31.0 | 4358 | 9 | AB014553 | AB014553 Homo sapl |
| 14 | 293.6 | 30.4 | 716 | 6 | AA083952 | AA083952 Sequence |
| 15 | 255.2 | 21.2 | 118361 | 2 | AC109383 | AC109383 Rattus no |
| 16 | 150.4 | 16.1 | 2240 | 9 | AK090492 | AK090492 Homo sapl |
| 17 | 152.6 | 15.8 | 2706 | 9 | IR05054 | IR05054 Homo sapl |
| 18 | 145.2 | 15.0 | 36230 | 9 | AF001059 | AF001059 Homo sapl |
| 19 | 145.2 | 15.0 | 39553 | 9 | AF001058 | AF001058 Homo sapl |
| 20 | 145.2 | 15.0 | 340000 | 9 | AF001753 | AF001753 Homo sapl |
| 21 | 60.4 | 6.3 | 1247 | 5 | GGCD80 | GGCD80 Homo sapl |
| 22 | 44.4 | 4.6 | 125020 | 9 | AF429315 | AF429315 Homo sapl |
| 23 | 41 | 4.2 | 290080 | 2 | AC096333 | AC096333 Rattus no |
| 24 | 40.2 | 4.2 | 125020 | 9 | AF429315 | AF429315 Homo sapl |
| 25 | 40.2 | 4.2 | 205050 | 10 | AI731853 | AI731853 Mouse DNA |
| 26 | 39.8 | 4.1 | 44553 | 9 | HS8085 | HS8085 Human DNA |
| 27 | 39.8 | 4.1 | 151796 | 2 | AC096595 | AC096595 Homo sapl |
| 28 | 39.8 | 4.1 | 177883 | 2 | AC046159 | AC046159 Homo sapl |
| 29 | 39.8 | 4.1 | 279011 | 9 | AEO06467 | AEO06467 Homo sapl |
| 30 | 39.6 | 4.1 | 73185 | 2 | AC069580 | AC069580 Homo sapl |
| 31 | 39.6 | 4.1 | 134091 | 2 | AC023349 | AC023349 Homo sapl |
| 32 | 39.6 | 4.1 | 142185 | 2 | AC002265 | AC002265 Homo sapl |
| 33 | 39.6 | 4.1 | 183784 | 2 | AC101948 | AC101948 Mus muscu |
| 34 | 38.8 | 4.0 | 2347 | 10 | MMY14334 | MMY14334 Mus muscu |
| 35 | 38.8 | 4.0 | 126243 | 3 | AC130997 | AC130997 Rattus no |
| 36 | 38.8 | 4.0 | 227035 | 2 | AC116585 | AC116585 Mus muscu |
| 37 | 38.8 | 4.0 | 261224 | 10 | AL645527 | AL645527 Mouse DNA |
| 38 | 38.6 | 4.0 | 127458 | 2 | AC119554 | AC119554 Rattus no |
| 39 | 38.6 | 4.0 | 174571 | 2 | AC106476 | AC106476 Rattus no |
| 40 | 38.4 | 4.0 | 1141 | 6 | AA083744 | AA083744 Sequence |
| 41 | 38.4 | 4.0 | 170700 | 2 | AC127469 | AC127469 Papio cyn |
| 42 | 38.4 | 4.0 | 173588 | 2 | AC127468 | AC127468 Papio cyn |
| 43 | 38.2 | 4.0 | 71320 | 2 | AC095614 | AC095614 Rattus no |
| 44 | 38.2 | 4.0 | 97902 | 9 | AL595618 | AL595618 Human DNA |
| 45 | 38.2 | 4.0 | 159468 | 2 | AC023314 | AC023314 Homo sapl |

ALIGNMENTS

| | | | | | | |
|------------|--|------------|--------|-----|--------|-----------------|
| RESULT 1 | AF216747 | AF216747 | 966 bp | RNA | linear | ROD 23-MAR-2000 |
| LOCUS | AF216747 | | | | | |
| DEFINITION | Mus musculus B7-related protein 1 mRNA, partial cds. | | | | | |
| ACCESSION | AF216747 | | | | | |
| VERSION | AF216747.1 | GI:7286510 | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Mus musculus | | | | | |
| ORGANISM | Mus musculus | | | | | |

REFERENCE
AUTHORS
1 (bases 1 to 966)
Yoshinaga, S.K., Whoriskey, J.S., Khare, S.D., Sarmiento, U., Guo, J.,
Horan, T., Shih, G., Coccia, M.A., Kohno, T.,
Tafiri-Bladt, A., Campbell, P., Chang, D., Chiu, L., Dai, T., Duncan, G.

| | | | |
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| OY | 61 | CCTCAGATTTCACAGGGGTTCTTTCCTGGCTCTTGCGTCTGTCTGCTGTTGACAC | 120 |
| Dd | 127 | CTCCATGTTTCTTAGGGGTTCTTTCTTGCTTGCTGCTGTCTGTTGAACAC | 186 |
| OY | 121 | CTCTGTGCCTCTGACAGACTAAGTGGGTGCATAGTGGGACGAAATGTGGTCTC | 180 |
| Dd | 187 | CTCTGTGCCTCTGACAGACTAAGTGGGTGCATAGTGGGACGAAATGTGGTCTC | 246 |
| OY | 181 | AGCTCATTTGACCCCCACAGACGCCATTTCAACTTGAAGTGGTCTGTATTTGGCAA | 240 |
| Dd | 247 | AGCTCATTTGACCCCCACAGACGCCATTTCAACTTGAAGTGGTCTGTATTTGGCAA | 306 |
| OY | 241 | ATCGAAAACCCGAAAGTTTCGGTGACTTAACACTGACCCTTACAAGCTCCAGGATCAAT | 300 |
| Dd | 307 | ATCGAAAACCCGAAAGTTTCGGTGACTTAACACTGACCCTTACAAGCTCCAGGATCAAT | 366 |
| OY | 301 | GTTGACAGTTCCTACAGAAMCAGGGGCCATCTGTCCCTGGACTGCATGAAGCAGGGTAAAC | 360 |
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| OY | 361 | TTCCTCTCTGTACCTGAAGATTCACCCCTCAGGATACCCAGAGTTCCATATGCCGGGTA | 420 |
| Dd | 427 | TTCCTCTCTGTACCTGAAGATTCACCCCTCAGGATACCCAGAGTTCCATATGCCGGGTA | 486 |
| OY | 421 | TTTTAATAATACAGCACAGAGTTAGTCAAGATCTTGGAAGAGTGGTCCGCTGGCTGTG | 480 |
| Dd | 487 | TTTTAATAATACAGCACAGAGTTAGTCAAGATCTTGGAAGAGTGGTCCGCTGGCTGTG | 546 |
| OY | 481 | GCAGCAAACTTCAGTACACCTGTCTCATCAGCACCTGTGATAGCTCCAAACCCGGGCCAGAA | 540 |
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| OY | 541 | CGTACCTACACCTGCATGTCCAAAGATGGCTTACCCAGAGCCCACCTGTATTGGATCAAC | 600 |
| Dd | 607 | CGTACCTACACCTGCATGTCCAAAGATGGCTTACCCAGAGCCCACCTGTATTGGATCAAC | 666 |
| OY | 601 | ACAAAGGCAATTAAGCTTAATAGACAGGGCTGCAAGAAATTAACATGTCCTACTTGAACAAAG | 660 |
| Dd | 667 | ACAAAGGCAATTAAGCTTAATAGACAGGGCTGCAAGAAATTAACATGTCCTACTTGAACAAAG | 726 |
| OY | 661 | TTGGGCTGTATGATGTATATCAGCACATTTAAGGCTCCCTTGGACATCTCTGGGGATGTT | 720 |
| Dd | 727 | TTGGGCTGTATGATGTATATCAGCACATTTAAGGCTCCCTTGGACATCTCTGGGGATGTT | 786 |
| OY | 721 | CTGTGCTGCGTATGAGAAATGTGGCTTCCAACGAACATCTACTAGCATTTAGCCAGCAGAA | 780 |
| Dd | 787 | CTGTGCTGCGTATGAGAAATGTGGCTTCCAACGAACATCTACTAGCATTTAGCCAGCAGAA | 846 |
| OY | 781 | AGTTTCACGTGGAAATTAACAAAGAAACCCACAGGAAACCAATAATATGATTAAGAAC | 840 |
| Dd | 847 | AGTTTCACGTGGAAATTAACAAAGAAACCCACAGGAAACCAATAATATGATTAAGAAC | 906 |
| OY | 841 | CTTGTCCTCCGCTCTGCTGTACTGGCGGACAGCGGCAATTCGTTCCCTGCATCATATACAGA | 900 |
| Dd | 907 | CTTGTCCTCCGCTCTGCTGTACTGGCGGACAGCGGCAATTCGTTCCCTGCATCATATACAGA | 966 |
| OY | 901 | CGCAGCGCTCCCAACCGAAGCTATACAGAGCCCAAGACTGTACAGCTTGAACCTTACAGAC | 960 |
| Dd | 967 | CGCAGCGCTCCCAACCGAAGCTATACAGAGCCCAAGACTGTACAGCTTGAACCTTACAGAC | 1026 |
| OY | 961 | CACGCC 966 | |
| Dd | 1027 | CACGCC 1032 | |
| <hr/> | | | |
| RESULT 3 | | | |
| AFI199027 | | | |
| LOCUS | AFI199027 | 2718 bp | mRNA linear ROD 17-FEB-2000 |
| DEFINITION | Mus musculus B7-1-like protein (GI50) | mrna, | complete cds. |
| ACCESSION | AFI199027 | | |
| VERSION | AFI199027.1 | | |
| KEYWORDS | | | |

| | |
|--|--|
| SOURCE | Mus musculus. |
| ORGANISM | Mus musculus. |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2718) |
| AUTHORS | Ling, Y., Wu, P.W., Finerley, H.F., Bean, K.M., Spaulding, V., Fouser, L.A., Leonard, J.P., Hunter, S.E., Zollner, R., Thomas, J.L., Miyashiro, J.S., Jacobs, K.A. and Collins, M. Cutting edge: identification of GL50, a novel B7-1-like protein that functionally binds to ICOS receptor J. Immunol. 164 (4), 1653-1657 (2000) |
| TITLE | |
| JOURNAL | J. Immunol. 164 (4), 1653-1657 (2000) |
| MEDLINE | 20126021 |
| PUBMED | 10657606 |
| REFERENCE | 2 (bases 1 to 2718) |
| AUTHORS | Ling, Y. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (26-OCT-1999) Immunology, Genetics Institute, 87 Cambridgepark Drive, Cambridge, MA 02140, USA |
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| BASE COUNT | 703 a 709 c 661 g 645 t |
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| Query Match | 100.0%; Score 966; DB 10; Length 2718; |
| Best Local Similarity | 100.0%; Pred. No. 1.6e-289; |
| Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| OY | 1 ATGCAGCTAAAGTGTCCCTGTTTGTGTGTCCTTGGGACACGAGCACTGTTGGAGAAG 60 |
| Db | 67 ATGCAGCTAAAGTGTCCCTGTTTGTGTGTCCTTGGGACACGAGCACTGTTGGAGAAG 126 |
| OY | 61 CTCCATGTTTTACCGGGTCTTTTCTGTGGTGGTCTGTCGTCTGTGAGCAGC 120 |
| Db | 127 CTCCATGTTTTACCGGGTCTTTTCTGTGGTGGTCTGTCGTCTGTGAGCAGC 186 |
| OY | 121 CTGTGTGCTGCCCTGCGAGAGACTGAAGTGGTGCATGTGGGCCAGCATGTGGCTC 180 |
| Db | 187 CTGTGTGCTGCCCTGCGAGAGACTGAAGTGGTGCATGTGGGCCAGCATGTGGCTC 246 |
| OY | 181 AGCGCATTTGACCCCCACAGAGCGCATTTCAAATTGATGGTCTGTATGCTATTGGCAA 240 |
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| OY | 241 ATCGAAAAACCGAAGATTTCGGTAGCTACTACTGCTTACAAGTCTCCAGGAGTCAAT 300 |
| Db | 307 ATCGAAAAACCGAAGATTTCGGTAGCTACTACTGCTTACAAGTCTCCAGGAGTCAAT 366 |
| OY | 301 GTGACAGTTTCTCTACAGAACAGGGGCATCTGTCCCTGAGACTGCATGAAAGAGGTAAAC 360 |
| Db | 367 GTGACAGTTTCTCTACAGAACAGGGGCATCTGTCCCTGAGACTGCATGAAAGAGGTAAAC 426 |
| OY | 361 TTCTCTGTGTACCTGAGAAATGTCAACCCTTCAGAGTAACCGAGAGTTCAATGCGGGGTA 420 |

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Db 427 TTCTCTGTACCTGGAAGATGTCACCCCTCAGATACCCAGAGATTACATGCCGGGTA 486
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QY 541 CGTACCTACACCTGTATCAGACACCTGTATAGCTCAACCCGGGCCAGAA 600
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Db 667 ACACGAGATATAGCCCAATAGACAGGCTCTGAGATATACACTGTCTATTGAACAA 726
QY 661 TTGGGCTGTATGATGTAATCAGACATTAAGGCTCCCTTGACATCTCGTGGGATGT 720
Db 727 TTGGGCTGTATGATGTAATCAGACATTAAGGCTCCCTTGACATCTCGTGGGATGT 786
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QY 961 CACGCC 966
Db 1027 CACGCC 1032

RESULT 4
BC029227 2803 bp mRNA linear ROD 07-AUG-2002
LOCUS BC029227
DEFINITION Mus musculus, lcos ligand, clone MGC:35971 IMAGE:4217333, mRNA,
complete cds.
VERSION BC029227.1 GI:22137738
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2803)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgapds-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu

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Gunaratne, P.H., Garcia, A.M., Lu, X., Huijck, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAC Plate: 61 Row: k Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7657219.

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BASE COUNT 715 a 746 c 682 g 660 t
ORIGIN

Query Match 100.0%; Score 966; DB 10; Length 2803;
Best Local Similarity 100.0%; Pred. No. 1,6e-289; Indels 0; Gaps 0;
Matches 966; Conservative 0; Mismatches 0;

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QY 61 CTCGATGTTTCTAGCGGGTCTTTTCTGTGCTGTGCTGTTCTGCTGTTGAGCAGC 120
Db 218 CTCGATGTTTCTAGCGGGTCTTTTCTGTGCTGTGCTGTTCTGCTGCTGTTGAGCAGC 277
QY 121 CTCTGTGCTGCTCTGTGAGAGACTGGAAGTGGTGCAATGTTGGGACAGCATGTGTCCTC 180
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[illegible]

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| Db | 241 | ATCGAAAAACCAGAAAGTTTGGTGACTTACTTACCTGGCTTCAAGAAGTCTCCAGGATCAAT | 300 |
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| Oy | 361 | TTCCTCTGTACTGGAAGATGTACCCCCCAGAGATTAACCCAGAGATTCACATCCCGGTA | 420 |
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| Db | 541 | CCTTACCTACACCTGCATGTGTCCAAAGATGGGTACCCAGAGCCCACCACTGTATTGGATCAAC | 600 |
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| Db | 601 | ACAACGCAAAATATGCTTAATATGACACAGGCTCTGACAAATTAACACTGTCTACTTGAACAAG | 660 |
| Oy | 661 | TTGGGCGCTTATGATATTAATACAGACATTAAAGGCTCCCTTGGACATCTGTGGGGATGTT | 720 |
| Db | 661 | TTGGGCGCTTATGATATTAATACAGACATTAAAGGCTCCCTTGGACATCTGTATGGGGATGTT | 720 |
| Oy | 721 | CTGTGCTGCGTAGAGATGTGGCTCTCCACAGAAATCACTAGTACATAGTACGACGACGAGAA | 780 |
| Db | 721 | CTGTGCTGCGTAGAGATGTGGCTCTCCACAGAAATCACTAGTACATAGTACGACGACGAGAA | 780 |
| Oy | 781 | AGTTTACATCGGAATATTAACCAAAAGAACCCACAGAGAAACCCACAAATATATAGTTAAAAGTC | 840 |
| Db | 781 | AGTTTACATCGGAATATTAACCAAAAGAACCCACAGAGAAACCCACAAATATATAGTTAAAAGTC | 840 |
| Oy | 841 | CTTGTCCCGCGTCTGTCTGTACTGGCGGAGCGGATTCGTTTCCCTTCAATCATATATACAGA | 900 |
| Db | 841 | CTTGTCCCGCGTCTGTCTGTACTGGCGGAGCGGATTCGTTTCCCTTCAATCATATATACAGA | 900 |
| Oy | 901 | CGCAGCGCTCCCGACCGAAGCTATACAGAGACCAAGACTGTACACCTTGAACTTACAGAC | 960 |
| Db | 901 | CGCAGCGCTCCCGACCGAAGCTATACAGAGACCAAGACTGTACACCTTGAACTTACAGAC | 960 |

RESULT 6
AF394451 1759 bp mRNA linear ROD 25 -JUL-2001

LOCUS Mus musculus B7-1like protein GL50-B (Icosl) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF394451
VERSION AF394451.1 GI:15011417

| | |
|---------------------------|---|
| SOURCE | Mus musculus. |
| ORGANISM | Mus musculus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| REFERENCE AUTHORS | 1 (bases 1 to 1759) Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F. and Collins M. |
| TITLE | Differential expression of inducible costimulator-lylgand splice variants: lymphoid regulation of mouse GL50-B and human GL50 molecules |
| JOURNAL | J. Immunol. 166 (12), 7300-7308 (2001) |
| MEDLINE | 21286479 |
| PUBMED | 11390480 |
| REFERENCE | 2 (bases 1 to 1759) |
| AUTHORS | Ling V., Wu P.W., Miyashiro J., Marusic S., Finnerty H.F. and Collins M. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (22-JUN-2001) Immunology, Genetics Institute/Wyeth Ayrst, 200 Cambridge Park Drive, Cambridge, MA 02140, USA |
| FEATURES | Location/Qualifiers |
| source | 1..1759 /organism="Mus musculus" /db_xref="taxon:10090" /note="3' RACE product" |
| gene | 1..1759 /gene="Icosl" /note="GL50-B; ICOS-L" |
| CDS | 1..1044 /gene="Icosl" /note="ICOS-lylgand splice variant" /codon_start=1 /product="B7-like protein GL50-B" /protein_id="AAK7544.1" /db_xref="GI:15011418" /translation="MOLEKPCFVSLGTRQPYWKKLHVSGFFSLGILFLLLSSLCASAA SAENRVLGVMSNVLSCLIDPBRHFNLSGLYVMOLENPEVSATYLKIPSPGINDV SSYNRGRLSDSMKOGNEFXLKNTVPDQDETCRENNALAEIKVLIIEEVYRLRV AANKSTPIVISTSDSNPROERTITCMKSNKPENPLNIWINTNSLIDTALONTYVILI NKLVLYDVISLRLPWTHSHGDVLLCCVEVALHONTISIQASEFTGNNTKNPOETHNN ELKLVLPVLAIAAFIVSFLLIRTPRHRSYTGPVKVILELTDMAPVPDYDLIPRP YLMSPCLETRLGLP" |
| BASE COUNT | 461 a 506 c 365 g 427 t |
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| Best Local Similarity | 99.8%; Pred. No.1.le-286; |
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| Db | 1 ATGCAGCTAAAGGCCCTGTGGTGCTTTGACCTGGGAACCGCAGCAGCTGTGGAAAG 60 1 ATGCAGCTAAAGTGCCTGTTTGTGTCCTTGGGACCGCAGCAGCTGTGGAAAG 60 |
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| Db | 61 CTCATGTTTTAGCGGGGTTCTTTCTGCTCTTGGTCTGTCTGCTGCTTTGAGACAC 120 |
| QY | 121 CTCTGTCGCTCTCTCTGCAAGACATGAAGCGGTGCAATGTGGGACGAAGAATGGGTCTC 180 121 CTCTGTCGCTCTCTCTGCAAGACATGAAGCGGTGCAATGTGGGACGAAGAATGGGTCTC 180 |
| Db | 121 CTCTGTCGCTCTCTCTGCAAGACATGAAGCGGTGCAATGTGGGACGAAGAATGGGTCTC 180 |
| QY | 181 AGCTGATTGACCCCCACAGAGCGCATTTCAACTTAGAGTGCTGTATCTATTTGGCAA 240 181 AGCTGATTGACCCCCACAGAGCGCATTTCAACTTAGAGTGCTGTATCTATTTGGCAA 240 |
| Db | 181 AGCTGATTGACCCCCACAGAGCGCATTTCAACTTAGAGTGCTGTATCTATTTGGCAA 240 |
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| Db | 301 GTGGACAGTTTCCACAAAGAACAGGGGCGAATGTCCTGAGCTCCATGAAGACAGGTAC 360 |
| QY | 361 TTCTCTCTCTACTGTAAGATGTACCCCTCAGAGATACCAGAGTTTCATGTCGGGTA 420 |

[illegible]

| Db | 254 | TGATGTACCCGGCCGGCATGCTGGGGGGGCGACTTCTCCCTGCGCTTGTTCACAGCACC | 313 |
|---------------------------|---|--|----------------------------|
| QY | 389 | CTCAGGATACCCAGAGTTCACATGCCGGGATATTATGATATACAGCCACAGATTAGTCA | 448 |
| Db | 314 | CCGAGGACAGACAGAAATTCATGCTGGTGT--TGAGCCAATCCCTGGGATTCAGG | 370 |
| QY | 449 | AGATCTTGGAGAGTGGTCAAGCTGGCTGTGGGACGAAACTTCAAGTACCTGGTCA | 508 |
| Db | 371 | AGTTTGTAGCGTTGAGGTTACACTGATGTGGGACGCAAACTTCAAGCGCTGCCGTGCA | 430 |
| QY | 509 | GCACCTCTGATAGCTCCAAACCCGGGCGCAGAAACGTACTTACCTGATATGCCAATG | 568 |
| Db | 431 | GGCGCCCGCCAGAGCCCTCCAGG--ATGAGCTACCTTACAGTGTACATCCATTAACG | 487 |
| QY | 569 | GCTACCCAGAGCCCAACTGTATTGGATCAACACAGSGACAAATACCTAATAGACAGG | 628 |
| Db | 488 | GCTACCCAGAGCCCAACTGTATTGGATCAATAGACGACAAACAGCCGTGCTGACAGG | 547 |
| QY | 629 | CTTGACAAATATACACTTCTACTTGAACAGTTGGGGCTGTATGATATATACACACAT | 688 |
| QY | 548 | CTGTGCAATATGACACCGCTTCTTGAACATCGGGGCTTGTATAGAGTGGTACCGTGC | 607 |
| Db | 689 | TAAAGCTCCCTTGGACATCTCGTGGGAGTGTTCGTGCTGCTAGACAGATGGCTTCC | 748 |
| Db | 608 | TGAGGATGCGAAGGACCCCGCAGCGAACAATGGCTGCTGATAGAACAGCGTTCGC | 667 |
| QY | 749 | ACCGACATACATCTATGACATTAGCCAGCGACGAAGTTTACTGTGGAATATACACAAAGC | 808 |
| Db | 668 | AGCAATACCTGATCTCGGACCGCAGACAGGAATGACATGCGAGAGAGACAGATCA | 727 |
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| Db | 728 | CAGAGATCCAGTCACTA | 745 |
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| LOCUS | AX100595 | 953 bp | DNA linear PAT 10-APR-2001 |
| DEFINITION | Sequence 5 from Patent WO0121796. | | |
| ACCESSION | AX100595 | | |
| VERSION | AX100595.1 | GI:13619598 | |
| KEYWORDS | | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 953) | | |
| AUTHORS | Ling, V. and Dunuss, J. Joannopolulos, K. | | |
| FILE | G150 molecules and uses therefor | | |
| JURNAL | Patent: WO 0121796-A 5 29-MAR-2001; | | |
| | GENETICS INSTITUTE, INC. (US) | | |
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| | VTPODEQKFLVLVSQSLGFEVLTVEVTLVAANFSVPVYSAHSPSODELFTCTSS | | |
| | INGPBRNVYVWINKTNSLIDALONDFELFMENGLDVVSLRLARPSVNICGIE | | |
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| | CRDKLQHSITAGAAVSPETLSTMSNLILLS" | | |
| BASE COUNT | 210 a | 277 c | 276 g 190 t |
| ORIGIN | | | |
| Query Match | 31.0%; | Score 299.6; | DB 6; Length 953; |
| Best Local Similarity | 64.8%; | Pred. No. 9e-82; | |
| Matches 478; Conservative | 0; | Mismatches 254; | Indels 6; Gaps 2; |

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| OY | 89 | GTTTGGCTGCTGTTCCTGGCGTGTTGAGCAGCCCTGTGGCTCTGCACAGACTGAAG | 148 |
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| Dd | 97 | TCAGAGCGATGGTAGTCAGCGCCGACGGAGCTTCAGCTGGCTGGCTGACCAAGAAGCCGTT | 156 |
| OY | 209 | TCAACTTGAGTGTGTGTATGTCTATTGGCAATATGCATAAACCCCAAACTTTCGGGACTT | 268 |
| Dd | 157 | TTGATTTTAAATGATTTTATCTATATTTGGCAACAACAGTGAGTGCAAAACCGTGTGACTT | 216 |
| OY | 269 | ACTTACCTGCTTATCAAGTCTCCAGGGAATCAATGTGGACAGTTCCTCCAAAGAACAGGGCC | 328 |
| Dd | 217 | ACCAATATCCCAAGAAACAGCTCTCTGGAAAAAGTGGACAGCGCGTACCGGAACCGAGCCC | 276 |
| OY | 329 | AATCTGCTCCCTGGACTTCATGAAGAGGGTAAGTCTTCTGTACTGAAAGATGTCAACC | 388 |
| Dd | 277 | TGATTTACACCGGCCCCGCGATGTGCGGGCGAGATCTTCCCTGGCGTTGTCAAACGTCACC | 336 |
| OY | 389 | CTCAGAGTATCCCGAGAGTTACATATCGCGGGATTATTAATATACAGCCACAGAGTTAGCA | 448 |
| Dd | 337 | CCCAAGSAGCAGAGAAGTTTCACTGCTGCTGTT---TAGCCAATCCCTGGGATTCAGG | 393 |
| OY | 449 | AGATCTTGGAAAGAGTGTGTGAGGTCGCTGTGGCAGCAAACTTCAATACACTGTCACTA | 508 |
| Dd | 394 | AGGTTTGTAGCTTGAAGTTTACATCTGATGTGGCAGCAAACTTCAAGCGTGCCTGCTCA | 453 |
| OY | 509 | GCACCTCTGATAGCTTCACAAACCGGGCCGAGGAAGTACACCTCACCGTCAATGTCAGATG | 568 |
| Dd | 454 | GGGCCCCCAGACCCCTCCACAG--ATGAGCTCACCTTACCGTGTATCATCAATAAACG | 510 |
| OY | 569 | GCTACCCAGAGGCCCAACCTGTATTGGATCAACACAGGACAAATAGCCTAATAGACACGG | 628 |
| Dd | 511 | GCTACCCAGAGGCCCAACCTGTATTGGATCAACACAGGACAAATAGCCTAATAGACACAG | 570 |
| OY | 629 | CTCTGCAATATTAACACTGTCTACTTGAAACAGTGGGCTCTGATATGTAATACACACAT | 688 |
| Dd | 571 | CTCTGCAATATTAACACTGTCTACTTGAAACAGTGGGCTCTGATATGTAATACACACAG | 630 |
| OY | 689 | TAAAGCTCCCTTGGACATTCGTGGGGAGTGTCTGTGCTGTAGAGATGTGGCTTCC | 748 |
| Dd | 631 | TGAGATGCGCAGAGAACCCCGACGCTGTAACATITGGCTGTGATAGAAAGCGTCTTGCG | 690 |
| OY | 749 | ACCAAGATCACTATGACATTAGCCACAGGCAAGATTTCACTGGAATATACACAAAGAAC | 808 |
| Dd | 691 | ACCAAGATCACTATGACATTAGCCACAGGCAAGATTTCACTGGAATATACACAAAGAAC | 750 |
| OY | 809 | CACAGGAACCCCAATA | 826 |
| Dd | 751 | CAGAGATCCAGTCACTA | 768 |
| RESULT 10 | | | |
| AF199028 | | 1009 bp | mRNA linear PRI 17-FEB-2000 |
| LOCUS | | | |
| DEFINITION | Homo sapiens B7-like protein (GL50) | mrna | complete cds. |
| ACCESSION | AF199028 | | |
| VERSION | AF199028.1 | GI:6983943 | |
| KEYWORDS | . | | |
| SOURCE | Homo sapiens. | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| REFERENCE | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| AUTHORS | 1 (bases 1 to 1009) Ling,V., Wu,P.W., Finerly,H.F., Bean,K.M., Spaulding,V., Fouser,L.A., Leonard,J.P., Hunter,S.E., Zollner,R., Thomas,J.L., Miyashiro,J.S., Jacobs,K.A. and Collins,M. Cutting edge: identification of GL50, a novel B7-like protein that functionally binds to ICOS receptor J. Immunol. 164 (4), 1653-1657 (2000) | | |
| JOURNAL | 20126021 | | |
| PUBMED | 10657606 | | |

Location/Qualifiers
1. .4358

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| Db | 736 | TGAGGATCGAGAGGAGGCCGCCACGCTGAAACATTTGGCTCTGTCATAGAGAAAGCGCTTCTTGC | 795 |
| Qy | 749 | ACCGAAGACATCTACTAGCATTTAGCCAGCGAGAAAGTTTCACTGTGAAATTAACACAAAGAAC | 808 |
| Db | 796 | AGCGAAACCTGACTGTCTGGCGCCAGACAGGAAATGACATCTCGAGAGAGAGACAAAGATCA | 855 |
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| Db | 856 | CAGAGAAATCCAGTCAGTA | 873 |

RESULT 14
AX083952

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| DEFINITION | Sequence 3 from Patent WO0112658. | DATE | 28-FEB-2001 |
| ACCESSION | AX083952 | | |
| VERSION | AX083952.1 | | |
| KEYWORDS | GI:13185509 | | |
| SOURCE | human. | | |
| ORGANISM | human. | | |

REFERENCE
Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 716)

ISIS INNOVATION LIMITED (GB)
 Location/Qualifiers
 Patent: WO 0112658-A 3 22-FEB-2001;
 human ICOS ligand and application thereof
 JOURNAL
 FEATURES
 Source

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BASE COUNT      164 a      206 c      201 g      145 t
ORIGIN          /organism="Homo sapiens"
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| Query Match | 30.4% | Score 293.6; | DB 6; | Length 716; |
| Best Local Similarity | 65.4%; | Pred. No. 6.5e-80; | | |
| Matches 463; | Conservative 0; | Mismatches 239; | Indels 6; | Gaps 2 |

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| QY | 149 | TCGGTGCAATGTGTGGGAGCAATGTGTCTCAGCTGATGTAACCCACAGACGCATT | 20 |
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| QY | 209 | TCACCTTGATGGTCTGTATGTCTATTGGCAATCGAAAAACGAGAACTTTCGGTGACTT | 26 |
| Db | 134 | TTGATTTAAATGATGTTTACGTATATTGGCAACACAGTAGTGAAACACGTGTGACT | 19 |
| QY | 269 | ACTACCTGCCTTCAAGTCTCCAGGATTCATATGGACACTTCTTCAGAAACAGAGGCC | 32 |
| Db | 194 | ACCACTATCCACAGAACACTCTTTGGAAAACTGTGCACACCGCTTACCGGAACCGAGGCC | 25 |
| QY | 329 | ATCTGCTCCCTGGAGCTCCATGAAGCAGGTTACTTCTCTGTACTGGAAGATGTCAACC | 38 |
| Db | 254 | TGATGTACCGCGCGGCACTGTGCGCGGCGCTTCTCCCTGCGCTTTTCAACGTCAACC | 31 |
| QY | 389 | CTCAGGATACCCAGAGATTCATATGCGGGGATTTTGAATACAGCACAGAGTTAGTCA | 44 |
| Db | 314 | CCGAGACGAGCGAAGATTTTCACTGCTCTGGTGT---TGAGCCAAATCCCTGGGAATTCAGG | 37 |
| QY | 449 | AGATCTTGGAAAGAGTGGTCAAGGCTGCGTGTGGCAGCAAACTTTCAGTACACTCTCATCA | 50 |
| Db | 371 | AGGTTTGTGCGCTTGAAGGTTCACTGTGATGTGGCAGCAAACTTTCAGGCTGCGCTCTCA | 43 |
| QY | 509 | GCACCTTGATAGTCCCAACCCGGGCGCAGGAACGTACTCAACCTGCATGTCCAAAGATG | 56 |
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23764 24834: contig of 1071 bp in length
24835 24934: gap of unknown length
24935 26287: contig of 1353 bp in length
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26388 27625: contig of 1238 bp in length
27626 27725: gap of unknown length
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30916 31015: gap of unknown length
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33145 35268: contig of 2124 bp in length
35269 35368: gap of unknown length
35369 36727: contig of 1359 bp in length
36728 36827: gap of unknown length
36828 38579: contig of 1752 bp in length
38580 38680: gap of unknown length
38681 40103: contig of 1424 bp in length
40104 40203: gap of unknown length
40204 41569: contig of 1366 bp in length
41570 41669: gap of unknown length
41670 43297: contig of 1628 bp in length
43298 43397: gap of unknown length
43398 44984: contig of 1587 bp in length
44985 45084: gap of unknown length
45085 46680: contig of 1596 bp in length
46681 46780: gap of unknown length
46781 47854: contig of 1074 bp in length
47855 47954: gap of unknown length
47955 50008: contig of 2054 bp in length
50009 50108: gap of unknown length
50109 52473: contig of 2367 bp in length
52476 52575: gap of unknown length
52576 53982: contig of 1407 bp in length
53983 54082: gap of unknown length
54083 56462: contig of 2380 bp in length
56463 56562: gap of unknown length
56563 57928: contig of 1366 bp in length
57929 58028: gap of unknown length
58029 58701: contig of 1673 bp in length
58702 59702: gap of unknown length
59703 61238: contig of 1437 bp in length
61239 61339: gap of unknown length
61340 63241: contig of 1903 bp in length
63242 63342: gap of unknown length
63343 64929: contig of 1588 bp in length
64930 65028: gap of unknown length
65029 66969: contig of 1940 bp in length
66970 67069: gap of unknown length
67070 68289: contig of 1220 bp in length
68290 68390: gap of unknown length
68391 70161: contig of 1772 bp in length
70162 70261: gap of unknown length
70262 72370: contig of 2109 bp in length
72371 72470: gap of unknown length
72471 74894: contig of 2424 bp in length
74895 74994: gap of unknown length
74995 76362: contig of 1368 bp in length
76363 76462: gap of unknown length
76463 78021: contig of 1559 bp in length
78022 78121: gap of unknown length
78122 79467: contig of 1346 bp in length
79468 79567: gap of unknown length
79568 82968: contig of 3401 bp in length
82969 83068: gap of unknown length
83069 85662: contig of 2594 bp in length
85663 85762: gap of unknown length
85763 87946: contig of 2184 bp in length
87947 88046: gap of unknown length
88047 89879: contig of 1833 bp in length
89880 89979: gap of unknown length
89980 91441: contig of 1462 bp in length

Query Match 21.2%; Score 205.2; DB 2; Length 118361;
Best Local Similarity 87.4%; Pred. No. 4e-52;
Matches 236; Conservative 0; Mismatches 33; Indels 1; Gaps 1;
OY 481 GCAGCAACTTCAGTACACCTGTCATCAGCACCCTGTATGCTCCCAACCCGGGCCAGGAA 540
|||||
DB 52095 GCAGCAAACTTCAGTACGCCCTGTATCAGCACCCTGTGCGACTCTGACCCCTGGCCAGGAA 52154
|||||
OY 541 GGTACCTACACCTGCATGTCACAGATGCTACCCAGAGCCCAACCTGTATTGATCAAC 600
|||||
DB 52155 GCACCTTCACCTGCATGTCACAGAAATGCTACCCAGAGCCCAACCTGTATTGATCAAC 52214
|||||
OY 601 ACAAGGACATATACCTAATATAGACAGGCTGTGACAAATTAACCTGTCTACTTGAACAAG 660
|||||
DB 52215 AGACGACATATACCTAATATAGACAGACTCTCAGAAATTAACAGGCTCTACTTGAACAAG 52274
|||||
OY 661 TTGGGCTGTATGATGTATATACACACATTAAGGCTCCCTTGACATCTGCTGGGATGTT 720
|||||
DB 52275 TTGGGCTGTATGATGACGTCGTACACACATGAGATCCCTTGACATCTGCTGGGATGTT 52333
|||||
OY 721 CTGTGCTGTAGAGAAATGCTGTCCAC 750
|||||
DB 52334 ATCTGCTGTAGAGAAATGCTGTCCAC 52363
|||||

Search completed: November 17, 2002, 04:44:04
Job time : 1953.37 secs


```

PR 03-FEB-1999; 99US-0244448.
PR 08-MAR-1999; 99US-0264527.
XX
XX (AMGE-) AMGEN INC.
XX
XX Yoshinaga SK:
XX
XX WPI: 2000-543476/49.
XX P-PSDB: AAB08725.
XX
XX Novel nucleic acids encoding the proteins CRP-1 and B7Rp1 are useful
XX in the treatment, prevention and diagnosis of T cell mediated disorders
XX
XX Claim 2: Fig 2A; 174pp; English.
XX
XX The present sequence encodes a B7Rp1 (B7 related protein-1)
XX polypeptide. The specification also describes a CRP1 (CD28 related
XX protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
XX activation, and represent a receptor-ligand pair. CRP1 and B7Rp1 are
XX predicted to be a type I transmembrane protein. The nucleic acids are
XX useful for regulating T cell activation or proliferation in an animal.
XX The polypeptides are useful for treating, preventing ameliorating or
XX diagnosing a T-cell mediated disorder in an animal. They can also be
XX used to identify test molecules that bind to the polypeptides.
XX
SQ Sequence 966 BP; 247 A; 256 C; 229 G; 234 T; 0 other;

Query Match 100.0%; Score 966; DB 21; Length 966;
Best Local Similarity 100.0%; Pred. No. 7.2e-298;
Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAGCTAAAGTCCCTTTGTCCTGGGACGACGCGCTTTGGAAGAG 60
DB 1 ATGCGAGCTAAAGTCCCTTTGTCCTGGGACGACGCGCTTTGGAAGAG 60
QY 61 CTCACATGTTCTAGCGGGTCTTTCTGCTGCTGCTCTTCTGCTGCTGAGCAGC 120
DB 61 CTCACATGTTCTAGCGGGTCTTTCTGCTGCTGCTCTTCTGCTGCTGAGCAGC 120
QY 121 CTCCTGCTGCTCTGTCACAGACTGAAGTCGTCATGTCGTCGTCGTCGTC 180
DB 121 CTCCTGCTGCTCTGTCACAGACTGAAGTCGTCATGTCGTCGTCGTCGTC 180
QY 181 AGCTGATGAGCCGCCACAGAGCCATTCACACTGAGTGTGATCTATTGGCAA 240
DB 181 AGCTGATGAGCCGCCACAGAGCCATTCACACTGAGTGTGATCTATTGGCAA 240
QY 241 ATCGAAAACCCAGAGTTCGTCATCTACCTGCTTACAGTCTCCAGGATCAAT 300
DB 241 ATCGAAAACCCAGAGTTCGTCATCTACCTGCTTACAGTCTCCAGGATCAAT 300
QY 301 GTGGAGAGTTCACAGAAAGAGCGGCATCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 GTGGAGAGTTCACAGAAAGAGCGGCATCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 TTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 TTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 TTTATGAATACAGCCACAGAGTTCAGTCTGGAAGAGTGTGCTGCTGCTGCTG 480
DB 421 TTTATGAATACAGCCACAGAGTTCAGTCTGGAAGAGTGTGCTGCTGCTGCTG 480
QY 481 GCAGCAACTTCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 GCAGCAACTTCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 CGTACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 CGTACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 ACAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

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DB 601 ACAGAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 TTGGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 TTGGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 721 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 781 AGTTTCACTGGAATATACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 840
DB 781 AGTTTCACTGGAATATACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 840
QY 841 CTTGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 CTTGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 GCGACGCGTCCCGCCAGGAGTATACAGAGCCAGAGCTGACCTGGAATTAACAGAC 960
DB 901 GCGACGCGTCCCGCCAGGAGTATACAGAGCCAGAGCTGACCTGGAATTAACAGAC 960
QY 961 CACGCC 966
DB 961 CACGCC 966

RESULT 2
ABK87592
ID ABK87592 standard; cDNA; 966 BP.
XX
XX ABK87592;
XX
XX 07-OCT-2002 (first entry)
XX
XX cDNA encoding murine B7 related protein-1 (B7Rp1).
XX
XX CD28 related protein-1; CRP1; T-lymphocyte costimulatory protein;
XX B7 related protein-1; B7Rp1; T-cell mediated disorder; hypersensitivity;
XX IGE-mediated disorder; allergy; sinus inflammation; immune disease;
XX graft survival; immune activation; asthma; cancer gene immunotherapy;
XX T-cell dependent B-cell mediated disease; leukemia; sarcoma; melanoma;
XX adenocarcinoma; prostate tumour; lung carcinoma; colon carcinoma; tumour;
XX viral infection; Hepatitis A virus; autoimmune disorder; psoriasis;
XX rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
XX diabetes; immunethrombocytopenic purpura; toxic shock syndrome;
XX bone marrow; organ transplantation; inflammatory bowel disease;
XX allsensitisation; blood transfusion; graft vs. host disease; mouse;
XX gene; ss.
XX
XX Mus musculus.
XX
XX OS
XX
XX Key 1, 966 location/Qualifiers
XX CDS /tag= a
XX FT /product= "B7Rp1"
XX FT /note= "B7 related protein-1"
XX FT /partial
XX FT /note= "No stop codon given"
XX
XX WO200244364-A2.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-US44859.
XX
XX 28-NOV-2000; 2000US-0728420.
XX
XX (AMGE-) AMGEN INC.
XX
XX (AMGE-) AMGEN CANADA INC.
XX
XX Yoshinaga SK, Mak TW, Shahinian A, Blatt AT, Senaldi G;

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XX WPI: 2002-547698/58.
 XX Novel isolated T-lymphocyte costimulatory polypeptide, such as CD28
 PT related protein-1 or B7 related protein-1, useful for treating,
 PT preventing or ameliorating a T-cell mediated disorder in an animal -
 PS Claim 2; Fig 2a; 197pp; English.
 XX
 CC The invention describes an isolated T-lymphocyte costimulatory
 CC polypeptide (I), such as CD28 related protein-1 (CRP1) or B7 related
 CC protein-1 (B7RP1), and orthologues, allelic variants or alternatively
 CC sliced variants of these sequences. (I) is useful for treating,
 CC preventing, ameliorating or diagnosing a T-cell mediated disorder or a
 CC susceptibility to a T-cell mediated disorder in an animal. (I) is useful
 CC for identifying a test molecule which binds to (I) by contacting (I) with
 CC a test molecule, and determining the extent of binding of (I) to the test
 CC molecule. The method further comprises determining the activity of (I)
 CC when bound to the compound. An anti-(I) antibody is useful for
 CC suppressing an immune response in an animal, for decreasing IgE
 CC production in an animal or for treating an IgE-mediated disorder such as
 CC asthma, allergies, hypersensitivity and sinus inflammation. (I) and
 CC anti-(I) antibodies are useful for treating immune disease, graft
 CC survival, immune activation, T-cell dependent B-cell mediated disease,
 CC cancer gene immunotherapy (for e.g. leukemias, sarcomas, melanomas,
 CC adenocarcinomas, prostate tumours, lung carcinomas, colon carcinomas and
 CC other tumours), viral infection (e.g. by Hepatitis A virus), autoimmune
 CC disorders (such as rheumatoid arthritis, psoriasis, multiple sclerosis,
 CC diabetes, systemic lupus erythematosus and immunethrombocytopenic
 CC purpura), toxic shock syndrome, bone marrow and organ transplantation,
 CC inflammatory bowel disease, allogeneic sensitisation due to blood transfusions,
 CC and the treatment of graft vs. host disease, and for regulating the
 CC interaction of B7RP1 or CRP1. This sequence encodes the murine B7
 CC related protein-1 (B7RP1) a novel protein of the T-cell costimulatory
 CC pathway.
 CC
 XX
 SQ Sequence 966 BP: 247 A; 256 C; 229 G; 234 T; 0 other;
 Query Match 100.0%; Score 966; DB 24; Length 966;
 Best Local Similarity 100.0%; Pred. No. 7, 2e-298;
 Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCAGTAAGTGTCCCTTTTGTGCTTGGGAACGAGCGCTGTTGGAAGAAG 60
 DB 1 ATGCAGTAAGTGTCCCTTTTGTGCTTGGGAACGAGCGCTGTTGGAAGAAG 60
 QY 61 CTCATGTTCTAGCGGGTCTTTTGTGCTTGGTCTGCTGTTGAGCAGC 120
 DB 61 CTCATGTTCTAGCGGGTCTTTTGTGCTTGGTCTGCTGTTGAGCAGC 120
 QY 121 CTCGTGCTGCTGCTGAGAGAGTGAAGTGGTGGCAAGTGGTGGCTC 180
 DB 121 CTCGTGCTGCTGCTGAGAGAGTGAAGTGGTGGCAAGTGGTGGCTC 180
 QY 181 AGCTGATTTGACCCCAAGAGCCCATTTCACTGATGCTATTTGGCAA 240
 DB 181 AGCTGATTTGACCCCAAGAGCCCATTTCACTGATGCTATTTGGCAA 240
 QY 241 ATGGAAGCCAGAGATTTGGTACTTACTTACCTCTTCAAGTCTCCAGGATCAAT 300
 DB 241 ATGGAAGCCAGAGATTTGGTACTTACTTACCTCTTCAAGTCTCCAGGATCAAT 300
 QY 301 GTGGAGATTTCCATCAAGAAAGGGGCAATCTCCCTGAGCTCCATGAAGAGGTAAAC 360
 DB 301 GTGGAGATTTCCATCAAGAAAGGGGCAATCTCCCTGAGCTCCATGAAGAGGTAAAC 360
 QY 361 TTCTCTCTGATGTAAGATGTACCCCTCAGAGATACCAGAGATTTACATGCGGGTA 420
 DB 361 TTCTCTCTGATGTAAGATGTACCCCTCAGAGATACCAGAGATTTACATGCGGGTA 420
 QY 421 TTTATATATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGGTCAAGGCTGGCTGTG 480
 DB 421 TTTATGAAATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGGTCAAGGCTGGCTGTG 480

QY 481 GCAGCAACTTACAGTACACCTGTATCAGACCTGTGATGCTCAACCCGGGCGAGAA 540
 DB 481 GCAGCAACTTACAGTACACCTGTATCAGACCTGTGATGCTCAACCCGGGCGAGAA 540
 QY 541 CGTACCTACACCTGTATGCTCAAGAAATGGCTACCCAGAGCCCAACCTGTATGATCAAC 600
 DB 541 CGTACCTACACCTGTATGCTCAAGAAATGGCTACCCAGAGCCCAACCTGTATGATCAAC 600
 QY 601 ACAAGGACATATGCTTAATAGACAGGCTCTGACATTAACCTGTACTTGAACAAG 660
 DB 601 ACAAGGACATATGCTTAATAGACAGGCTCTGACATTAACCTGTACTTGAACAAG 660
 QY 661 TTGGGCTGTATGATGATTAATACACACATTAAGGCTCCCTTGACATCTGTGGGATGTT 720
 DB 661 TTGGGCTGTATGATGATTAATACACACATTAAGGCTCCCTTGACATCTGTGGGATGTT 720
 QY 721 CTGTGCTGCTGAGAGATGTGCTTCCACAGACATCATTAGATGAGCCAGAA 780
 DB 721 CTGTGCTGCTGAGAGATGTGCTTCCACAGACATCATTAGATGAGCCAGAA 780
 QY 781 AGTTTACAGGAATATACCAAGAACCCAGAGAACCAATATAGTTAAAGTC 840
 DB 781 AGTTTACAGGAATATACCAAGAACCCAGAGAACCAATATAGTTAAAGTC 840
 QY 841 CTGTGCCGCTCTTCTGCTACTGCGGCGAGCGCATTTGTTCTTCATCATATACAGA 900
 DB 841 CTGTGCCGCTCTTCTGCTACTGCGGCGAGCGCATTTGTTCTTCATCATATACAGA 900
 QY 901 CGACAGCGTCCCGACGGAAGCTATACAGACCCAGAGCTGTACAGTTACATTACAGAC 960
 DB 901 CGACAGCGTCCCGACGGAAGCTATACAGACCCAGAGCTGTACAGTTACATTACAGAC 960
 QY 961 CACGCC 966
 DB 961 CACGCC 966
 RESULT 3
 AAF79919
 ID AAF79919 standard; DNA; 2718 BP.
 XX
 AC AAF79919;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Nucleotide sequence of a murine GL50-1.
 XX
 KW GL50: antigen; antigen presenting cell; T cell proliferation; tumour;
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
 KW acquired immune deficiency syndrome; AIDS; vaccine; ss.
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 67..1035
 FT /*tag= a
 FT /*product= "GL50"
 FT sig_peptide 67..195
 FT /*tag= b
 XX
 PN W0200121796-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US25892.
 XX
 PR 21-SEP-1999; 99US-0155043.
 XX
 PA (GBV) GENETICS INST INC.
 XX
 PI Ling V, Dunussl-Joannopolulos K;
 XX

DR WPI: 2001-244938/25.
P-PSDB: AAB67711.

XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
XX
PS Claim 1; Fig 1; 195pp; English.

XX The present sequence encodes a murine GL50-1 polypeptide. GL50
CC molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory
CC receptor ligands on T cells. GL50 modulating agents are used to
CC modulate an immune response in a subject. GL50 polypeptides are used
CC to modulate T cell costimulation, and to reduce the proliferation of
CC a tumour cell. Diseases that can be treated using GL50 molecules are
CC graft-versus-host disease, autoimmune disease, allergies, acquired
CC immune deficiency syndrome (AIDS), and viral infections. The GL50
CC molecules can be used in vaccines. GL50 polynucleotides can be used
CC to locate gene regions associated with genetic disease, in tissue
CC typing, and in forensic identification of a biological sample.

Sequence 2718 BP; 703 A; 709 C; 661 G; 645 T; 0 other:

Query Match 100.0%; Score 966; DB 22; Length 2718;
Best Local Similarity 100.0%; Pred. No. 1.3e-297;
Matches 966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGCAGCTAAAGTGTCCCTGTTTGTGCTTGGGAACAGCAGCCTTTGGAAGAG 60
DB ATGCAGCTAAAGTGTCCCTGTTTGTGCTTGGGAACAGCAGCCTTTGGAAGAG 126
OY 61 CTCACATGTTTACGGGGGTTTCTTCTGCTGCTGCTTCTGCTGCTGCTGCTGCTG 120
DB 127 CTCACATGTTTACGGGGGTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 186
OY 121 CTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 187 CTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
OY 181 ACCTGATTTAGACCCCGACAGAGCCATTTCAACTGAGTGTGCTGATTTGAGCA 240
DB 247 ACCTGATTTAGACCCCGACAGAGCCATTTCAACTGAGTGTGCTGATTTGAGCA 306
OY 241 ATCGAAGAACCCAGAAAGTTTGGTGAATCTACTGCTTACAGTCTCCAGGATCAAT 300
DB 307 ATCGAAGAACCCAGAAAGTTTGGTGAATCTACTGCTTACAGTCTCCAGGATCAAT 366
OY 301 GTGAGCAGTTTCTCAAGAAAGAGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 367 GTGAGCAGTTTCTCAAGAAAGAGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
OY 361 TTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 427 TTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
OY 421 TTTATGAATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGCTGAGGCTGCTG 480
DB 487 TTTATGAATACAGCCACAGAGTTAGTCAAGATCTTGAAGAGGTGCTGAGGCTGCTG 546
OY 481 GCGAGCAAACTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 547 GCGAGCAAACTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
OY 541 CGTACCTACAGCTGATGCTCAAGATGCTTACCCAGAGCCCAACTGATTTGATCAAC 600
DB 607 CGTACCTACAGCTGATGCTTCAAGATGCTTACCCAGAGCCCAACTGATTTGATCAAC 666
OY 601 ACAAGCGAATAGCTTAATAGACAGCGCTCTGCAAGATTAACCTGCTACTTGAACAAG 660
DB 667 ACAAGCGAATAGCTTAATAGACAGCGCTCTGCAAGATTAACCTGCTACTTGAACAAG 726
OY 661 TTGGGCTGTATGATGATTAATACGACATTAAGGCTCCCTGGACATCTGCTGGGATGTT 720
DB 727 TTGGGCTGTATGATGATTAATACGACATTAAGGCTCCCTGGACATCTGCTGGGATGTT 786
OY 721 CTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 787 CTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
OY 781 AGTTTCACCTGGAATTAACACAAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 840
DB 847 AGTTTCACCTGGAATTAACACAAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 906
OY 841 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 907 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966
OY 901 CGCAGCGCTGCCACCGAAGCTATACAGGACCCAGACCTGACCTGGAATTAACAGC 960
DB 967 CGCAGCGCTGCCACCGAAGCTATACAGGACCCAGACCTGACCTGGAATTAACAGC 1026
OY 961 CACGCC 966
DB 1027 CACGCC 1032

DB 727 TTGGGCTGTATGATGATTAATACGACATTAAGGCTCCCTGGACATCTGCTGGGATGTT 786
OY 721 CTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 787 CTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
OY 781 AGTTTCACCTGGAATTAACACAAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 840
DB 847 AGTTTCACCTGGAATTAACACAAAGAACCCACAGAAACCCACAAATATAGTTAAAGTC 906
OY 841 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 907 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966
OY 901 CGCAGCGCTGCCACCGAAGCTATACAGGACCCAGACCTGACCTGGAATTAACAGC 960
DB 967 CGCAGCGCTGCCACCGAAGCTATACAGGACCCAGACCTGACCTGGAATTAACAGC 1026
OY 961 CACGCC 966
DB 1027 CACGCC 1032

RESULT 4
AAAF79920
ID AAFF79920 standard; DNA; 1759 BP.
XX
AC AAFF79920;
XX
DT 11-JUN-2001 (first entry)
XX
DE Nucleotide sequence of a murine GL50-2.
XX
KW GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine; ss.
XX
OS Mus musculus.
XX
FH
FT CDS
FT
FT Location/Qualifiers
CDS 1..1044
FT /tag= a
FT /product= "GL50"
XX
XX WO200121796-A2.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000MO-US25892.
XX
PR 21-SEP-1999; 99US-0155043.
XX
PA (GENY) GENETICS INST INC.
XX
PI Ling V, Dunussi-Joannopolulos K;
XX
XX WPI: 2001-244938/25.
XX P-PSDB: AAB67712.
XX
XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
PT
PS Claim 1; Fig 2; 195pp; English.

The present sequence encodes a murine GL50-2 polypeptide. GL50
CC molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory
CC receptor ligands on T cells. GL50 modulating agents are used to
CC modulate an immune response in a subject. GL50 polypeptides are used
CC to modulate T cell costimulation, and to reduce the proliferation of
CC a tumour cell. Diseases that can be treated using GL50 molecules are
CC graft-versus-host disease, autoimmune disease, allergies, acquired
CC immune deficiency syndrome (AIDS), and viral infections. The GL50

CC molecules can be used in vaccines. GL50 polynucleotides can be used
 CC to locate gene regions associated with genetic disease, in tissue
 CC typing, and in forensic identification of a biological sample.

XX Sequence 1759 BP; 461 A; 506 C; 365 G; 427 T; 0 other;

Query Match 99.0%; Score 956.8; DB 22; Length 1759;

Best Local Similarity 99.8%; Pred. No. 8.8e-295;

Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 ATGACAGCTAAAGTGTCCCTGTTTGTCTTGGGAACGAGCGCCTGTTGGAAAG 60
    |||||||
DB 1 ATGACAGCTAAAGTGTCCCTGTTTGTCTTGGGAACGAGCGCCTGTTGGAAAG 60
OY 61 CTCACATGTTCTAGCGGGTCTTTCTGGCTGTGTCTTCTTCTGCTGCTTGAGCAGC 120
    |||||||
DB 61 CTCACATGTTCTAGCGGGTCTTTCTGGCTGTGTCTTCTTCTGCTGCTTGAGCAGC 120
OY 121 CTCCTGCTGCTCTCTGACAGACTGAAGTGGTGGCAATGGTGGCAAGTGGTGTCTC 180
    |||||||
DB 121 CTCCTGCTGCTCTCTGACAGACTGAAGTGGTGGCAATGGTGGCAAGTGGTGTCTC 180
OY 181 AGCTGATTTGACCCCGACAGACGCCATTTTCACATTGAGTGTCTATTTGGCAA 240
    |||||||
DB 181 AGCTGATTTGACCCCGACAGACGCCATTTTCACATTGAGTGTCTATTTGGCAA 240
OY 241 ATGGAAGAACCCAGAAATTTCTGGTACTTACTACTGCTTACAAAGTCTCAGGAGTCAAT 300
    |||||||
DB 241 ATGGAAGAACCCAGAAATTTCTGGTACTTACTACTGCTTACAAAGTCTCAGGAGTCAAT 300
OY 301 GTGGACAGTTCTCTACAAAGACAGGGGCATCTGCTCCGTGACATTCATGAAGCAGGGTAA 360
    |||||||
DB 301 GTGGACAGTTCTCTACAAAGACAGGGGCATCTGCTCCGTGACATTCATGAAGCAGGGTAA 360
OY 361 TTCTCTCTGCTGCTGAGAAATGTCAACCCCTCAGAGTATCCAGAGATTTACATGCCGGGTA 420
    |||||||
DB 361 TTCTCTCTGCTGCTGAGAAATGTCAACCCCTCAGAGTATCCAGAGATTTACATGCCGGGTA 420
OY 421 TTTATGAAATACAGCCACAGATTTAGTCAAGATCTTGGAGAGGTGGTCAAGGCTGCTG 480
    |||||||
DB 421 TTTATGAAATACAGCCACAGATTTAGTCAAGATCTTGGAGAGGTGGTCAAGGCTGCTG 480
OY 481 GCAGCAAACTTCTAGTACCTGTATCAGACCTGTGATAGTCAACCCGGGCGAGAA 540
    |||||||
DB 481 GCAGCAAACTTCTAGTACCTGTATCAGACCTGTGATAGTCAACCCGGGCGAGAA 540
OY 541 CGTACCTACACCTGTATGCTCAAGAAATGGCTACCCAGAGGCCCAACCTGTATTTGGATCAAC 600
    |||||||
DB 541 CGTACCTACACCTGTATGCTCAAGAAATGGCTACCCAGAGGCCCAACCTGTATTTGGATCAAC 600
OY 601 ACAAGGACAAATAGCCTAATAGACAGCGCTCTGACAGAAATACACTGTCTACTTGAACAAG 660
    |||||||
DB 601 ACAAGGACAAATAGCCTAATAGACAGCGCTCTGACAGAAATACACTGTCTACTTGAACAAG 660
OY 661 TTGAGGCTGTATGATGTAATCAGACATTTAAGGCTCCCTGGACATCTGCTGGGGAGTTT 720
    |||||||
DB 661 TTGAGGCTGTATGATGTAATCAGACATTTAAGGCTCCCTGGACATCTGCTGGGGAGTTT 720
OY 721 CTGTGCTGCTAGAGATGTGCTCTCCACAGACATCACTAGCATTTAGCCAGGAGAA 780
    |||||||
DB 721 CTGTGCTGCTAGAGATGTGCTCTCCACAGACATCACTAGCATTTAGCCAGGAGAA 780
OY 781 AGTTTACAGTGAATAAACAAGAAACCCAGAGAAACCCCAATATATGATTTAAAGTTC 840
    |||||||
DB 781 AGTTTACAGTGAATAAACAAGAAACCCAGAGAAACCCCAATATATGATTTAAAGTTC 840
OY 841 CTGTGCTGCTGCTGCTGATGAGGCGGAGGCAATTTGTTCTTCAATCATATACAGA 900
    |||||||
DB 841 CTGTGCTGCTGCTGCTGATGAGGCGGAGGCAATTTGTTCTTCAATCATATACAGA 900
OY 901 CGCAGCGTGTCCCGACGAAAGCTATACAGAGCCAGAGCTGTACAGCTTGAACCTTACAGAC 960
    |||||||
DB 901 CGCAGCGTGTCCCGACGAAAGCTATACAGAGCCAGAGCTGTACAGCTTGAACCTTACAGAC 960

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RESULT 5
AAE79942
ID AAE79942 standard; DNA; 1830 BP.
XX
AC AAE79942;
XX
DT 11-JUN-2001 (first entry)
XX
DE Nucleotide sequence of mGL50-mig2am fusion protein.
XX
KW GL50: antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine; ss.
XX
OS Synthetic.
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 26..1716
FT FT /*tag= a
FT FT /note= "contains introns"
FT FT 26..842
FT FT /*tag= b
FT FT 843..951
FT FT /*tag= c
FT FT 952..1281
FT FT /*tag= d
FT FT 1282..1393
FT FT /*tag= e
FT FT 1394..1716
FT FT /*tag= f
FT FT /*number= "3"
XX
PN WO200121796-A2.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-US25892.
XX
PR 21-SEP-1999; 99US-0155043.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Ling V, Dunussi-Joannopoulos K;
XX
DR WPI: 2001-244938/25.
XX
DR P-PSDB: AAB67719.
XX
PT New isolated nucleic acid encoding a GL50 polypeptide for modulating a
XX immune response and reducing the proliferation of a tumour cell -
XX
PS Disclosure: fig 29A; 195pp; English.
XX
XX
XX The present sequence encodes a fusion protein, comprising murine GL50
XX (mg50) and murine IgG2a (mig2a). The fusion protein is used in the
XX course of the invention. The specification describes GL50 polypeptides.
XX GL50 molecules are antigens on the surface of antigen presenting cells,
XX which costimulate T cell proliferation and bind to costimulatory receptor
XX ligands on T cells. GL50 modulating agents are used to modulate an immune
XX response in a subject. GL50 polypeptides are used to modulate T cell
XX costimulation, and to reduce the proliferation of a tumour cell. Diseases
XX that can be treated using GL50 molecules are graft-versus-host disease,
XX autoimmune disease, allergies, acquired immune deficiency syndrome
XX (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
XX GL50 polynucleotides can be used to locate gene regions associated with
XX genetic disease, in tissue typing, and in forensic identification of a
XX biological sample.

```

xx Sequence 1830 BP; 512 A; 498 C; 433 G; 387 T; 0 other;
sq

| | | | | |
|-----------------------|--------------|---------------------|---------------|--------------|
| Query Match | 71.6%; | Score 691.4; | DB 22; | Length 1830; |
| Best Local Similarity | 99.9%; | Pred. No. 5.8e-210; | | |
| Matches 692; | Conservative | 0; | Mismatches 1; | Indels 0; |
| | | | | Gaps 0; |

| | | | |
|----|-----|--|-----|
| OY | 139 | GAGACGTAAGCGGTGCAAAAGTGGGGACGAAGTGGTGCACAGTCGACATGACCCCGAC | 198 |
| | | | |
| Db | 101 | GAGCTGAAGTCGGTGCAAATGGTGGGAGCAATGGTGTCTACGTCGATTTGACCCCGAC | 160 |
| | | | |
| OY | 199 | AGAGCCATTTCACCTTGAGTGGTGTATGTATTTGGCAAAATCCAAACCGAGAATT | 258 |
| | | | |
| Db | 161 | AGAGCCATTTCACCTGAGTGGTGTATGTATTTGGCAAAATCCAAACCGAGAATT | 220 |
| | | | |
| OY | 259 | TGCGTACTTACTACCTGCCTTACAAGTCTCCAGGGATCAATGTGGACAGTTCTCTCAAG | 318 |
| | | | |
| Db | 221 | TGCGTACTTACTACCTGCCTTACAAGTCTCCAGGGATCAATGTGGACAGTTCTCTCAAG | 280 |
| | | | |
| OY | 319 | AACAGGGGGCCATCTGCCCTGGAGTCCATTAACAGAGGTAACTTCTCTGTACCTCGAAG | 378 |
| | | | |
| | 281 | AACAGGGGGCCATCTGTCTCTGGAGTCCATTAACAGAGGTAACTTCTCTGTACCTCGAAG | 340 |
| | | | |
| OY | 379 | AATGTCAACCCCTCAGATTACCCAGAGATTACATGCGCGGTATTTAATGATACGCACAC | 438 |
| | | | |
| Db | 341 | AATGTCAACCCCTCAGATTACCCAGAGATTACATGCGCGGTATTTAATGATACGCACAC | 400 |
| | | | |
| OY | 439 | GAGTTAGTCAAGATCTTGGAGAAGGTGTCAAGCTGCGTGTGGCAGCAAACTTCAGTAGAC | 498 |
| | | | |
| Db | 401 | GAGTTAGTCAAGATCTTGGAGAAGGTGTCAAGCTGCGTGTGGCAGCAAACTTCAGTAGAC | 460 |
| | | | |
| OY | 499 | CCGTGTCATCAGCACTCTGATAGTCTCAACCCGGGGCAGAAAGTACTACACCTGATG | 558 |
| | | | |
| Db | 461 | CCGTGTCATCAGCACTCTGATAGTCTCAACCCGGGGCAGAAAGTACTACACCTGATG | 520 |
| | | | |

| | |
|----------|-----------------------------------|
| RESULT 6 | |
| ABL35026 | |
| ID | ABL35026 standard; cDNA; 2729 BP. |

| | |
|----|---|
| AC | ABLJ3502b; |
| XX | |
| DT | 04-APR-2002 (first entry) |
| XX | |
| DE | Rat CDNA isolated from skin cells SEQ ID NO: 555. |
| XX | |
| KW | Human; rat; mouse; skin cell; skin wound; cancer; growth defect; |
| KW | developmental defect; inflammatory disease; dermatological; vulnary; |
| KW | immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene |
| KM | ss. |
| XX | |
| OS | Rattus sp. |
| XX | |

PN W0200190357-A1

PD 29-NOV-2001

PF 24-MAY-2001; 2001WO-NZ00099.

PR 24-MAY-2000; 2000US-206650P.

[illegible][illegible]

XX
F1, WALSON JD, STEELMAN W, CHURCH A, WALSON JR, RUMBLE ND

DR WP1; 2002-122020/16
DR P-PSDB; ABB72340.

XX
PT

PT growth and developmental defects, inflammatory diseases, or for

modulating immune responses -

PS Claim 1; Page 344-345; 466pp; English.
XY

CC The present invention provides the pro
CC isolated from human, murine and rat al

CC can be used in the development of therapeutic agents useful in the

CC defects, developmental defects and inflammatory diseases. The proteins

CC and cell-cell interaction, in maintaining tissue integrity, in wound

CC CDNA of the invention.

Sequence 2729 BP; 657 A; 761 C; 683 G; 628 T; 0 other;

| | | | | |
|-------------|--------|--------------|--------|--------------|
| Query match | 55.7%; | Score 538.2; | DB 24; | Length 2729; |
|-------------|--------|--------------|--------|--------------|

Best local similarity: 75.00; Area: no: 0.00 101;
Matches 723; Conservative 0; Mismatches 168; Indels 24; Gaps

QY 73 AGCGGTTCTTTCTGCTCTGGTCTGTCGTCTGCTGCTGTTGAGCAGCCCTCTGTGCTGCC 132

Db 158 AACAGGTTCTTTCCGGCTGCTGTTTTCCTGCTAATTTGCAGTCTCTGTGCGAG 217

133 TCTGCAGAGACTGAAGTCGGTGCATGTGTGGGCAGCAATGTGGTCTCAGCTGCATTGAC 192

Dh 218 GCTGAAGTTAAAGAGTCAATGCTGGGAGCGATGTGAGCTCCGCTGCATTAT 277

| | | | | |
|-----------------------|-----------------|---------------------|------------|--------------|
| Query Match | 55.7%; | Score 538.2; | DB 24; | Length 2729; |
| Best Local Similarity | 79.0%; | Pred. No. 6.6e-161; | | |
| Matches 723; | Conservative 0; | Mismatches 168; | Indels 24; | Gaps 6 |

| | | | |
|----|-----|---|-----|
| QY | 73 | AGGGGCTCTTTTGTGGCGTTGGCCGTCCTTGCTGGTGAACACCCTGTGGTGC | 132 |
| Db | 158 | AACAGGTTCTTTTCCGGTCCTGGTCTGTTTTGCTGCTATTTTGGCATGTCCTGTGGCAG | 217 |
| QY | 133 | TCTGACAGACTGGAAGTCGCGATGGTGGGACGAACTGTGGTGCACCTGCATTGAC | 192 |
| Db | 218 | GCTGAAGTTAAGAAGTCAATGCATGSGTGGGAGCATGTGGAGCTCCGCTGGTTAT | 277 |
| QY | 193 | CCCCACAGACGCCATTTTCACCTTGAGTGTCTGATGTCTATTGGCAA---TCGAAAAC | 249 |
| Db | 278 | CCTGGAGAAACCATTTCCAGCTTGGAATGATCTGTATGCTACTAGGGCAAACTGTCGATGAA | 337 |
| QY | 250 | CCAGAGAGTTGGGAGACTTACTACTCTG-----CTTACAAGTCTCCAGGGATCAATG | 303 |
| Db | 338 | GCTAAACCTGGTGAGCGATTATACCTGCCAGTCTCAACGAGCTTTCGAAATTCATGTG | 397 |
| QY | 304 | GACAGTTCTCTACAGAACAGGGGGCATCTGTGCCCTGTGACTCATGAGACGGGTAATTC | 363 |
| Db | 398 | AGCAACTCTCTACAGAACAGGGGCCCATCTGTGCACCGGAACTCATGAAGAAGGCGACTTC | 457 |
| QY | 364 | TCTCTGTACCTGAAGAAATGTCACCCCTCAGAGATACCCAGGAGTTTACATGCCGGGTATTT | 423 |
| Db | 458 | TCCCTGACACTGAGAAATGTCAACCCCTCAGAGATACCCAGGAGTTTCAAGTGTCTTGTCTTT | 517 |
| QY | 424 | ATGAATACAGCCACAGAGTTTAGTAAATCTTGGAAAGAGTGGTCAGAGCTGCTGTGGCA | 483 |
| Db | 518 | AGG---ATGTGTCACAGTTTAGGCAAAAGCCTTTGGAAAGAGTGGTCAGACACTGCTGTGGCA | 574 |
| QY | 484 | GCAAACTTCAGTATACCGTGCATCAGGACCTGTATAGTCTCAACCCGGGSCCAGAAAGT | 543 |
| Db | 575 | GCAAACTTCAGTACCGCTGTATATAGCACACTCTTGGCAGCTCTGACCCCTGGCCAGAAAGC | 634 |
| QY | 544 | ACCTACACCTGCACTGTCCAAAGAAATGGCTACCCACAGAGCCCAACCTGTATTGGATCAACACA | 603 |

Db 635 ACCTTCACTTGATGTCACAGATGGCTACCCAGAGCCCAACTGTATGTGATCAACAG 694
QY 604 AGGACAAATACCTTAATAGACACGGCTCTGCAAGATAACACTGTCTACTTGAAACAGTTG 663
Db 695 ACGGACAAATACCTTAATAGACAGACTCTGCAAGATAAAGCGGTCTACTTGAAACAGAGTTG 754
QY 664 GGCGTGTATGATGTAATACAGACATTAAGGCTCCCTTGGACATCTCGTGGGATGTTCTG 723
Db 755 GGCGTGTATGACGTCTGACACACTAGAGATCCCTTGGACACCCCAATGTGGATGTTATC 814
QY 724 TGTGCTGATAGAAATGTGGCTCTCCACAGAACATCACTACATTAACAGGAGAAAGT 783
Db 815 TGTGCTGATAGAAATGTGGCTCTCCACAGAACATCACTACATTAACAGGAGAAAGT 874
QY 784 TTTCACTGGA---AATAACACAAGAACCCACAGAGAAACCAATTAATGATTAAGATC 840
Db 875 TTTCACTGGAAGACACAGACAGAGAGCCACAGAGAAATCAACAGAGAGGCTACAAAGTGC 934
QY 841 CTGTGCTCCCGCTTGTGCTATGCTGGGCAAGCGCATTCCTTCTTCATCA-----TA 894
Db 935 CTTTTTCACGCGCTTGTGCTGACCTTCTGCGGTAGTGTGATTTTCATTCATCTGCTG 994
QY 895 TACAGACACAGCAG---CGTCCCAACCGAAGCTATACAGAGCCCAAGACTGTACAGCTTGA 951
Db 995 TACAGATGACAGGCGCTGCTCCCTGACAGAGCTATACAGAGCCCAAGGCTGTACAGCTTGA 1054
QY 952 CTTCACACACACAGCC 966
Db 1055 CTCACAGACCATTC 1069

RESULT 7

AAAA3831 standard; cDNA; 545 BP.

AAAA3831:

21-AUG-2000 (first entry)

Mouse secreted expressed sequence tag SEQ ID NO:406.

Human; mouse; chicken; rat; secreted expressed sequence tag; SESR;
expressed sequence tag; EST; probe; chemotactic; proliferative;
immunomodulatory; haematopoietic; chemokine; analgesic; haemostatic;
thrombolytic; antiinflammatory; cytoskeletal; antibacterial; antifungal;
antiviral; antidiabetic; antiaschmatic; vulnerrary; antiparkinsonian;
cerebroprotective; neuroprotective; nootropic; antipsoriasis;
vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
Klinefelter's syndrome; burn; osteoporosis; osteoarthritis;
central nervous system disorder; Alzheimer's disease; stroke;
Parkinson's disease; Huntington's disease; coagulation disorder;
haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
tumour; infection; depression; psoriasis; ss.

Mus musculus.

MO200021991-A1.

20-APR-2000.

15-OCT-1999; 99WO-US24206.

15-OCT-1998; 98US-0104436.

(GENY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR;

DR WPI; 2000-317938/27.

PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (SESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders -
PS Claim 1; Page 309; 803pp; English.

CC AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC sequence tags (SESTs). Isolated from human, mouse, chicken and rat
CC tissue sources. The SESTs can have a range of activities depending on
CC the tissues they were isolated from. The activities include:
CC chemotactic; proliferative; immunomodulatory; haematopoietic;
CC chemokine; analgesic; haemostatic; thrombolytic; antiinflammatory;
CC cytoskeletal; antibacterial; antifungal; antidiabetic;
CC antiaschmatic; vulnerrary; antiparkinsonian; neuroprotective;
CC nootropic; antiparkinsonian; antipsoriasis; cerebroprotective;
CC anticonvulsant; and antidepressant. The SESTs can be used for gene
CC therapy and in vaccines. The SESTs are useful as probes for the
CC identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the SESTs. Proteins encoded by the SESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC in the exemplification of the present invention.

SO Sequence 545 BP; 117 A; 151 C; 138 G; 138 T; 1 other:

Query Match 46.6%; Score 450.6; DB 21; Length 545;
Best Local Similarity 98.9%; Pred. No. 2; 6e-133;
Matches 453; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACGCTAAGTGTCCCTTTTGTGCTCTTGGAAACGACGCGCTTTGGAAAG 60
Db 87 ATGACGCTAAGTGTCCCTTTTGTGCTCTTGGAAACGACGCGCTTTGGAAAG 146
QY 61 CTCGATGTTCTAGCGGGTCTTTTGTGCTGTGCTGCTTGTGCTGTGACAGC 120
Db 147 CTCGATGTTCTAGCGGGTCTTTTGTGCTGTGCTGCTTGTGCTGTGACAGC 206
QY 121 CTGTGTGCTGCTCTCTGACAGACTGAGTGTGCAATGTGGGACCAATGTGCTC 180
Db 207 CTGTGTGCTGCTCTCTGACAGACTGAGTGTGCAATGTGGGACCAATGTGCTC 266
QY 181 AGCTGATGACCCCGACAGACCCATTTCACTTGAAGTGTGCTATTTGGCAA 240
Db 267 AGCTGATGACCCCGACAGACCCATTTCACTTGAAGTGTGCTATTTGGCAA 326
QY 241 ATGAAACCCCAAGATTTGCGTACTTACTCTCTTCAAGTCTCAGAGATCAAT 300
Db 327 ATGAAACCCCAAGATTTGCGTACTTACTCTCTTCAAGTCTCAGAGATCAAT 386
QY 301 GTGACAGTTCTTACAAAGACAGGGCCATCTGTCCCTGACTCCATGAAGAGGTAAC 360
Db 387 GTGACAGTTCTTACAAAGACAGGGCCATCTGTCCCTGACTCCATGAAGAGGTAAC 446
QY 361 TTTCTCTGTACTGAAAGATGTCACCCCTCAGAGATACCCAGAGATTCAGCCGGTA 420
Db 447 TTTCTCTGTACTGAAAGATGTCACCCCTCAGAGATACCCAGAGATTCAGCCGGTA 506
QY 421 TTTATGAATACAGCCACAGAGTTAGTCAAGATCTTGA 458
Db 507 TTTATGAATACAGCCACAGAGTTAGTCAAGATCTTGA 544

RESULT 8
AAA64556 standard; DNA; 864 BP.

[illegible][illegible]


```

Db      37  GTCTGGACGCTCTTCTCTGCTCTTTCAGCAGCCTTCAGCTGATCTCAGAGAAAGGAG 96
Qy      149  TCGGTGCAATGTGTGGCAGCAATGTGTGCTCAGCTGATTCAGTCCCGCCAGACGGCAT 208
Db      97  TCAAGGCAATGTGTAGCAGCAGCTGAGAGTCAAGTCCGCTTCCCTGAAGAGACCGTT 156
Qy      209  TCAACTGTAGTGGTGTATGTCTATTTGGCAATTCGAAACCCAGAGTTTGGTGACT 268
Db      157  TTGATTTAAATGATGTTTACGTATATTTGGCAACCAAGTACGTGAAACCCGTGTACCT 216
Qy      269  ACTACCTGCTTACAGTCTCCAGGATCAATGTGAGCAAGTTCCTCAAGACAGAGGCC 328
Db      217  ACCACATCCCAAGAACAGTCTTGGAAACGTGACGCGCTTACCGGAACCGAGGCC 276
Qy      329  ATCTGTCCCTGAGCTCAGTGAAGCAGAGGTTACTCTCTGTGATCTGAAGAAATGTACCC 388
Db      277  TGAATGTACCGCGCGGAGTGTCCGGGGGAGCTTCTCCCTGGCTTGTTCACAGTCAACC 336
Qy      389  CTCAGGATACCCAGAGTTCACATGCGCGGTATTTATGAAATACAGCCACAGAGTTAGTCA 448
D      337  CCCAGGACGAGAGAGATTCTCACTGCTGTGT---TGAGCCAAATCCCTGGGGATTTCAGG 393
Qy      449  AGATCTGGAAGAAGTGTGTGAGCTGCTGCTGTCGAGCAAACTTCAGTACACCTGTATCA 508
Db      394  AGGTTTGTAGCTGTGAGGTTACATGCTGATGTGCAAGCAAACTTCAGCGCGCGCTGTCA 453
Qy      509  GCACCTCTGTATAGCTCCAAACCCGGGCGCAGAGTACCTACACCTGCAATGCCAAGATG 568
Db      454  GGGCCCCCAGAGCCCTCCAGG---ATGAGCTTACCTTCACTGATCAATCCATTAACG 510
Qy      569  GGTACCCAGAGCCCAACCTGTATTTGGATCAACACAGAGCAATAGCCTAATAGACAGG 628
Db      511  GGTACCCAGAGCCCAACCTGTATTTGGATCAATAGACAGCAATAGCCTAATAGACAGG 570
Qy      629  CTCTCAGAAATACCTGTCTACTGTAGAACAGTTGGGCTGTATGATGTAATCAACAT 688
Db      571  CTCTCAGAAATACCTGTCTACTGTAGAACAGTTGGGCTGTATGATGTAATCAACAT 630
Qy      689  TAAAGCTCCCTTGACATCTGTGTGGGATGTTCTGTGCTGCTGAGAAATGTGCTGTC 748
Db      631  TGAGGATGCGACGCGACCCCGAGCGTGAACATTTGGCTGTGCTGATAGACAGCTGTTTGC 690
Qy      749  ACCGAAATCACTAGCTTATAGCCAGCAGAAATTTCACTGGAATTAACAAAGAAC 808
Db      691  AGCAGAACTACTGTGTGCGCAGCAGAGGAAATGACATCGAGAGAGAGACAAAGATCA 750
Qy      809  CACAGGAAACCCACATA 826
C      751  CAGAGAAATCCAGTCAGTA 768

```

RESULT 12

AA64557 ID AA64557 standard; DNA: 1294 BP.

AC AAA64557;

DT 02-JAN-2001 (first entry)

DE DNA sequence encoding a human B7RP1 polypeptide.

XX CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;

KM T-lymphocyte activation; type I transmembrane protein; T cell activation;

XX T cell proliferation; T cell mediated disorder; ss.

OS Homo sapiens.

FH Key 1..199 Location/Qualifiers

FT 5'UTR /tag= a

FT CDS 200..1108

FT /tag= b

```

FT      sig_peptide 200..247 /product= "B7RP1"
FT      mat_peptide 248..1105 /tag= c
FT      /tag= d
PN      W0200046240-A2.
PD      10-AUG-2000.
PE      27-JAN-2000; 2000MO-US01871.
PR      03-FEB-1999; 99US-0244448.
PR      08-MAR-1999; 99US-0264527.
XX      (AMGE-) AMGEN INC.
PI      Yoshinaga SK.
PI      WPI: 2000-543476/49.
DR      P-PSDB: AAB08729.
XX
PT      Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
PT      in the treatment, prevention and diagnosis of T cell mediated disorders
PS
XX      Claim 2: Fig 12A; 174bp; English.
XX
XX      The present sequence encodes a B7RP1 (B7 related protein-1)
XX      polypeptide. The specification also describes a CRP1 (CD28 related
XX      protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
XX      activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
XX      predicted to be a type I transmembrane protein. The nucleic acids are
XX      useful for regulating T cell activation or proliferation in an animal.
XX      The polypeptides are useful for treating, preventing ameliorating or
XX      diagnosing a T-cell mediated disorder in an animal. They can also be
XX      used to identify test molecules that bind to the polypeptides.
SQ      Sequence 1294 BP; 262 A; 400 C; 392 G; 240 T; 0 other;
Query Match 31.0%; Score 299.6; DB 21; Length 1294;
Best Local Similarity 64.8%; Pred. No. 7.7e-85;
Matches 478; Conservative 0; Mismatches 234; Indels 6; Gaps 2;
Qy      89  GTCTGTGCTGTTCTTCTGCTGCTGTGAGCAGCCTTGTGCTGCTTGCAGACACTGAG 148
Db      213  GTCTGTGCTGCTTCTTCTGCTTCTCAGCAGCCTTGCAGCTGATCTAGAGAAAGAG 272
Qy      149  TCGGTGCAATGTGTGGCAGCAATGTGTGCTCAGCTGATTCAGTCCCGCCAGACGGCAT 208
Db      273  TCAAGGCAATGTGTAGCAGCAGCTGAGAGTCAAGTCCGCTTCCCTGAAGAGACCGTT 332
Qy      209  TCAACTGTAGTGGTGTATGTCTATTTGGCAATTCGAAACCCAGAGTTTGGTGACT 268
Db      333  TTGATTTAAATGATGTTTACGTATATTTGGCAACCAAGTACGTGAAACCCGTGTACCT 392
Qy      269  ACTACCTGCTTACAGTCTCCAGGATCAATGTGAGCAAGTTCCTACAGAAAGAGAGGCC 328
Db      393  ACCACATCCCAAGAACAGTCTTGGAAACGTGACGCGCTTACCGGAACCGAGGCC 452
Qy      329  ATCTGTCCCTGAGCTCAGTGAAGCAGGTTACTCTCTGTGATCTGAAGAAATGTACCC 388
Db      453  TGAATGTACCGCGCGGAGTGTCCGGGGGAGCTTCTCCCTGGCTTGTTCACAGTCAACC 512
Qy      389  CTCAGGATACCCAGAGTTCACATGCGCGGTATTTATGAAATACAGCCACAGAGTTAGTCA 448
Db      513  CCCAGGACGAGAGAGATTCTCACTGCTGTGT---TGAGCCAAATCCCTGGGATTTCCAG 569
Qy      449  AGATCTGGAAGAAGTGTGTGAGCTGCTGCTGTCGAGCAAACTTCAGTACACCTGTATCA 508
Db      570  AGGTTTGTAGCTGTGAGGTTACATGCTGATGTGCAAGCAAACTTCAGCGCGCGCTGTCA 629
Qy      509  GCACCTCTGTATAGCTCCAAACCCGGGCGCAGAGTACCTACACCTGCAATGCCAAGATG 568

```


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OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 01:50:50 ; Search time 1399.38 Seconds
(without alignments)
11179.834 Million cell updates/sec

Title: US-09-728-421D-6

Sequence: 1 atgcagcctaaagcttcctcctc.....ttgaactacagaccagcgc 966

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 467.2 | 48.4 | 872 | 12 | BF580455 602097224 |
| 2 | 465 | 48.1 | 663 | 10 | BB612511 BB612511 |
| 3 | 454 | 47.0 | 694 | 10 | BB227026 BB227026 |
| 4 | 434 | 44.9 | 661 | 10 | BB638093 BB638093 |
| 5 | 410 | 42.4 | 538 | 9 | AI614037 AI614037 |
| 6 | 316.6 | 32.8 | 577 | 10 | BB637248 BB637248 |

| 7 | 298 | 30.8 | 962 | 9 | AL560774 |
|----|-------|------|------|----|----------|
| 8 | 297 | 30.7 | 440 | 9 | AA510455 |
| 9 | 296.4 | 30.7 | 1083 | 14 | BM923293 |
| 10 | 281.6 | 29.2 | 978 | 13 | BM543561 |
| 11 | 219 | 22.7 | 816 | 13 | BI488470 |
| 12 | 164 | 17.0 | 496 | 10 | AM753046 |
| 13 | 163 | 16.9 | 486 | 10 | AM377686 |
| 14 | 151.6 | 15.7 | 422 | 14 | R23544 |
| 15 | 147.2 | 15.2 | 476 | 12 | BE776710 |
| 16 | 130 | 13.5 | 663 | 10 | BB637811 |
| 17 | 113.8 | 11.8 | 448 | 10 | AM377683 |
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| 19 | 63.8 | 6.6 | 771 | 13 | BI911468 |
| 20 | 57.8 | 6.0 | 475 | 12 | BE603992 |
| 21 | 53.2 | 5.5 | 674 | 13 | BI393131 |
| 22 | 39.4 | 4.1 | 417 | 10 | AM445859 |
| 23 | 39.4 | 4.1 | 936 | 17 | CNS04667 |
| 24 | 38.8 | 4.1 | 837 | 12 | BE730328 |
| 25 | 38.2 | 4.0 | 518 | 9 | AI788059 |
| 26 | 38.2 | 4.0 | 578 | 9 | AI449399 |
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| 30 | 37.2 | 3.8 | 710 | 9 | AJ453546 |
| 31 | 37 | 3.8 | 718 | 9 | AJ446897 |
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| 38 | 36.8 | 3.8 | 645 | 13 | BM439415 |
| 39 | 36.8 | 3.8 | 691 | 9 | AJ450167 |
| 40 | 36.8 | 3.8 | 702 | 9 | AJ449834 |
| 41 | 36.8 | 3.8 | 717 | 9 | AJ448384 |
| 42 | 36.8 | 3.8 | 725 | 9 | AJ451418 |
| 43 | 36.8 | 3.8 | 730 | 9 | AJ446899 |
| 44 | 36.8 | 3.8 | 734 | 9 | AJ452616 |
| 45 | 36.8 | 3.8 | 788 | 9 | AJ446332 |

ALIGNMENTS

RESULT 1
BF580455
LOCUS 872 bp mRNA EST 12-DEC-2000
DEFINITION 602097224F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4217333 5',
mRNA sequence.
ACCESSION BF580455
VERSION BF580455.1 GI:11654167
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM9795 row: P column: 06
High quality sequence start: 2
High quality sequence stop: 670.
Location/Qualifiers

| Query Match | Best Local Similarity | Matches | Score | DB | Length |
|-------------|---|---------|---------------|-----|--------|
| 1 | ATGCAGCTAAAGTGTCCCTGTTTGTGTC -TTGGAGAACAGCAGCCGTTTGGAGAA | 59 | 48.4%; 86.0%; | 12; | 872; |
| 157 | ATGCAGCTAAAGTGTCCCTGTTTGTGTC -TTGGAGAACAGCAGCCGTTTGGAGAA | 216 | 0; 0; | 83; | 17; |
| 60 | GCTCATGTTTACAGGGTCTTTTGTGCTTGTGCTGTTCTGTTGCTTGAACAG | 119 | 0; 0; | 83; | 17; |
| 217 | GCTCATGTTTACAGGGTCTTTTGTGCTTGTGCTGTTCTGTTGCTTGAACAG | 276 | 0; 0; | 83; | 17; |
| 120 | CCTGTGCTGCTGTGAGAGATGAAATGCGTCAATGTTGGGAGAGATGCTGT | 179 | 0; 0; | 83; | 17; |
| 277 | CCTGTGCTGCTGTGAGAGATGAAATGCGTCAATGTTGGGAGAGATGCTGT | 336 | 0; 0; | 83; | 17; |
| 180 | CAGTGCATTCACCCACAGCCGATTCACATTGAGTGTGATGTCTA -TTGGC | 238 | 0; 0; | 83; | 17; |
| 337 | CAGTGCATTCACCCACAGCCGATTCACATTGAGTGTGATGTCTA -TTGGC | 396 | 0; 0; | 83; | 17; |
| 239 | AAATGAAACCCAGAGTTTGTGAGTCTTACTCTGCTTACCAAGTCCAGGATCA | 298 | 0; 0; | 83; | 17; |
| 397 | AAATGAAACCCAGAGTTTGTGAGTCTTACTCTGCTTACCAAGTCCAGGATCA | 456 | 0; 0; | 83; | 17; |
| 299 | ATGTGAGAGTCTTACCAAGAGGGGCGATCTGTCCCTGGACTCCATGAAGAGGTA | 358 | 0; 0; | 83; | 17; |
| 457 | ATGTGAGAGTCTTACCAAGAGGGGCGATCTGTCCCTGGACTCCATGAAGAGGTA | 516 | 0; 0; | 83; | 17; |
| 359 | ACTTGTCTGTACTGAAAGATGTACACCC -TCAGAGATCCAGAGTTCACATGCCG | 417 | 0; 0; | 83; | 17; |
| 517 | ACTTGTCTGTACTGAAAGATGTACACCCCTTCAGAGATCCAGAGTTCACATGCCG | 576 | 0; 0; | 83; | 17; |
| 418 | GTAATTATG -AATACAGCCACAG -AGTAGTCACAGATCTTGGAA - -GAGGTGTGACGC | 472 | 0; 0; | 83; | 17; |
| 577 | GTAATTATGAAATACAGCCACAGCAGTAGTAGTACAGATCTTGGAGAGGATGTGTCAGGC | 636 | 0; 0; | 83; | 17; |
| 473 | TGCGGTGTGGACCA - - - - -AATTCAGTACACCTGTATCATGACACCTGTATAGTCTCA | 526 | 0; 0; | 83; | 17; |
| 637 | TGCGGTGTGGACCACTTACAGTAAACCTGTGTATCATGACACCTGTATAGTCTCA | 696 | 0; 0; | 83; | 17; |
| 537 | ACCCGGCCAGAGAGTACTTACACCTGATCTTCAAGAAAGTCTACAGAGCCCAAC | 586 | 0; 0; | 83; | 17; |
| 697 | ACCCGGCCAGAGAGTACTTACACCTGATCTTCAAGAAAGTCTACAGAGCCCAAC | 756 | 0; 0; | 83; | 17; |
| 587 | TGTATTGATCAACAGAGGATAGCTTATATAGACAGG - -CTTGCAGATTAACA | 643 | 0; 0; | 83; | 17; |
| 757 | TGTATTGATCAACAGGATAGCTTATATAGACAGG - -CTTGCAGATTAACA | 816 | 0; 0; | 83; | 17; |
| 644 | CTGTCTACTTGAACAGTTGGGCTGTATGATGTATACAGCACCATTAGAGCTCC | 697 | 0; 0; | 83; | 17; |
| 817 | TGCTTACTGACACAGTTGGGCTGTATGATGTATACAGCACCATTAGAGCTCC | 870 | 0; 0; | 83; | 17; |

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| VERSION | B8612511.1 | GI:16453443 |
| KEYWORDS | EST. | |
| SOURCE | house mouse. | |
| ORGANISM | Mus musculus | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | |
| AUTHORS | 1 (bases 1 to 663) | |
| TITLE | Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okito,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tsurumi,T., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y. | |
| JOURNAL | RIKEN Mouse ESTs (Arakawa,T., et al. 2001) | |
| COMMENT | Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216 Email: genome-res@gscc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagl,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamamaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues. | |
| FEATURES | Location/Qualifiers | |
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| | /strain="C57BL/6J" | |
| | /db_xref="taxon:10090" | |
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| | /clone_lib="RIKEN full-length enriched, 0 day neonate skin" | |
| | /sex="mixed" | |
| | /tissue_type="skin" | |
| | /dev_stage="0 day neonate" | |
| | /lab_host="DH10B" | |
| | /note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' | |
| | GAAAGACAGACATCCAGAGCTCTTTTCTTTTCTTTTNN 3'] cDNA was prepared by using Trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization | |

to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGAGAGAGATTCGCGATTAAATTAATCCCGCCCC 3'. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC 1"

BASE COUNT 145 a 192 c 165 g 158 t 3 others

Query Match 48.1%; Score 465; DB 10; Length 663;
Best Local Similarity 99.2%; Pred. No. 1.1e-131;
Matches 476; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 179 ATGAGCTAAAGTCCCTGTTTGTCTCTTGGGAACGAGCCTGTTGGAAGAG 238
Y 61 CTCATGTTTCTACGGGGTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 239 CTCATGTTTCTACGGGGTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298
Y 121 CTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 299 CTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 358
Y 181 AGTGCATGACCCCGACAGCCGATTTCACTTGAGTGTCTGTATGTCTATTGGCAA 240
DB 359 AGTGCATGACCCCGACAGCCGATTTCACTTGAGTGTCTGTATGTCTATTGGCAA 418
Y 241 ATCGAAACACAGAGATTTGGTGGTCTTACTTCTGCTGCTGCTGCTGCTGCTGCTG 300
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Y 301 GTGACAGTCTCTACAGAAACAGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 479 GTGACAGTCTCTACAGAAACAGGGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 538
Y 361 TTCCTCTGATGAGTGAATGTACCCCTGAGATACCCAGAGTCCACATGCGGGGTA 420
DB 539 TTCCTCTGATGAGTGAATGTACCCCTGAGATACCCAGAGTCCACATGCGGGGTA 598
Y 421 TTATGATATACAGCAGATAGTATGATCAATCTTGGAGAGTGTGCTGCTGCTGCTG 480
DB 599 TTATGATATACAGCAGATAGTATGATCAATCTTGGAGAGTGTGCTGCTGCTGCTG 657

RESULT 3
BB272026 694 bp mRNA linear EST 23-OCT-2001
ORIGIN BB272026 RIKEN full-length enriched, adult male aorta and vein mus

ACCESSION BB272026
VERSION BB272026.2 GI:16354067
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 694)

REFERENCE
AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koyama, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyata, T., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
On Jul 3, 2000 this sequence version replaced gi:8897671.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuoka, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

source
1. 694
Location/Qualifiers
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/db_xref="taxon:10090"
/clone_id="A530099011"
/clone_1db="RIKEN full-length enriched, adult male aorta and vein"
/tissue_type="aorta and vein"
/sex="male"
/dev_stage="adult"
/note="Site-1: Salt; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGATTCGCGATTAAATTAATCCCGCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC 1."

BASE COUNT 190 a 177 c 158 g 169 t

ORIGIN

Query Match 47.0%; Score 454; DB 10; Length 694;
Best Local Similarity 98.9%; Pred. No. 2.6e-128;
Matches 457; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Y 468 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
DB 1 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60

| DB | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM | REFERENCE | AUTHORS |
|-----------|---------|---|-----------|---------|----------|--------|----------|-----------|---------|
| OY | 528 | CCGGGCGCAGAGAGCTACTCTACCTACCTGCATGTCGCAAGAAATGGCTCCAGACGCCAACCT | 587 | | | | | | |
| Db | 61 | CCCGGCGCAGAGAGCTACTCTACCTACCTGCATGTCGCAAGAAATGGCTCCAGACGCCAACCT | 120 | | | | | | |
| OY | 588 | GTATTGGATTCACAACACAGAGACATAGCCTTAATTAACACGCGCTCGCAGAAATACACTGT | 647 | | | | | | |
| Db | 121 | GTATTGGATTCACAACACAGAGACATAGCCTTAATTAACACGCGCTCGCAGAAATACACTGT | 180 | | | | | | |
| OY | 648 | CTACTTGAACAAGTTGGGCGCTGTATGATGTAAATCAGCACATTTAAAGCTCCCTTGGACATC | 707 | | | | | | |
| Db | 181 | CTACTTGAACAAGTTGGGCGCTGTATGATGTAAATCAGCACATTTAAAGCTCCCTTGGACATC | 240 | | | | | | |
| OY | 708 | TCGTGGGATGTCTGTCTGCTGTAGAGAAATCTGGCTCTCCACCGAATCATCAGCAT | 767 | | | | | | |
| Db | 241 | TCGTGGGATGTCTGTCTGCTGTAGAGAAATCTGGCTCTCCACCGAATCATCAGCAT | 300 | | | | | | |
| OY | 768 | TAGCCAGCAGCAAAATTTTCACGTGAATTAACCAAGAACCCACAGAAACCCACAAATTA | 827 | | | | | | |
| Db | 301 | TAGCCAGCAGCAAAATTTTCACGTGAATTAACCAAGAACCCACAGAAACCCACAAATTA | 360 | | | | | | |
| Db | 828 | TGAGTTAAAAGTCCTTGTCCCGCTCTGCTGTACTGGCGCAGCGGCATTCGTTCTT | 887 | | | | | | |
| OY | 361 | TGAGTTAAAAGTCCTTGTCCCGCTCTGCTGTACTGGCGCAGCGGCATTCGTTCTT | 420 | | | | | | |
| OY | 888 | CATCATATACAGAGCAGCGCGTCCCGCAGGAGCATACAG | 929 | | | | | | |
| Db | 421 | CATCATATACAGAGCAGCGCGTCCCGCAGGAGCATACAG | 462 | | | | | | |
| RESULT 4 | B638093 | B638093 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA A630008D12 5', mRNA sequence. | | | | | | | |
| ACCESSION | B638093 | B638093.1 GI:16473797 | | | | | | | |
| VERSION | B638093 | | | | | | | | |
| KEYWORDS | | EST. | | | | | | | |
| SOURCE | | house mouse. | | | | | | | |
| ORGANISM | | Mus musculus | | | | | | | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | | | | |
| AUTHORS | | 1 (bases 1 to 661) | | | | | | | |
| | | Arkawa, T., Carinci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nemura, K., Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. | | | | | | | |
| | | RIKEN Mouse ESTs (Arkawa, T., et al. 2001) | | | | | | | |
| | | Unpublished (2001) | | | | | | | |
| | | Contact: Yoshihide Hayashizaki | | | | | | | |
| | | Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute | | | | | | | |
| | | The Institute of Physical and Chemical Research (RIKEN) | | | | | | | |
| | | 1-7-22 Saitoh-cho, Tsukuba-shi, Ibaraki, 305-3858, Japan | | | | | | | |
| | | Tel: 81-45-503-9222 | | | | | | | |
| | | Fax: 81-45-503-9216 | | | | | | | |
| | | Email: genome-res@sc.riken.go.jp, | | | | | | | |
| | | URL: http://genome.res.riken.go.jp/ | | | | | | | |
| | | Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | | | | | | | |
| | | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) | | | | | | | |
| | | wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. | | | | | | | |
| | | RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer. Genome Res. 10 (11), 1757-1771 (2000) | | | | | | | |
| | | Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carinci, P., Sugahara, | | | | | | | |

| | Y. | and Hayashizaki,Y. | Computer-based methods for the mouse full-length cDNA |
|---------------------------|-------|---|---|
| | | | encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) |
| | | Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamana,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. | |
| | | | Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) |
| | | | Please visit our web site (http://genome.gsc.riken.go.jp) for further details. |
| | | e mouse tissues. | |
| FEATURES | | location/qualifiers | |
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| | | /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGGAGAAGACATCCACAGAGCTTTTGTTCCTTTTAAATTAAATTAATCCCCCCCCCCC 3'], cDNA was cleaved with XhoI and BamHI. Vector: a modified pluscript KS(+) after bulk excision from LambdaFLC I." | |
| BASE COUNT | 140 a | 191 c | 165 g |
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| Best Local Similarity | | 96.4%; | Pred. No. 3.7e-122; |
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| Oy | 1 | ATGCAGCTAAAGTGTCCTCGTTTTGTGTCCTTTGGAGACCAGCACCTGTTTGAAGAG | 60 |
| Dd | 168 | ATGCAGCTAAAGTGTCCTCGTTTTGTGTCCTTTGGAGACCAGCACCTGTTTGAAGAG | 227 |
| Oy | 61 | CTCCATGTTTTACAGGGGTTCTTTCTGTGTGTGTCTGTCTGTCTGTGTGACAGC | 120 |
| Dd | 228 | CTCCATGTTTTACAGGGGTTCTTTCTGTGTGTGTGTCTGTCTGTGTGTGAGCAGC | 287 |
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| Dd | 288 | CTCTGTGTCCTCGTCGACAGACTCAAGTCGGTGTGAATGNTGGCAGACAATGTGCTC | 347 |
| Oy | 181 | AGCTCATTTGACCCGCCACAGACGCCATTTCAACTTGAGTGTCTGTATGTCTATTGGCAA | 240 |
| Dd | 348 | AGCTCATTTGACCCGCCACAGACGCCATTTCAACTTGAGTGTCTGTATGTCTATTGGCAA | 407 |
| Oy | 241 | ATCGAAAACCCGAGAG-TTTGGTAGCTTACTACTGCTTCCTTACAGTCTCCAGGATCAA | 299 |
| Dd | 408 | ATCGAAAACCCGAGAGTTTGGTAGCTTACTACTGCTTCCTTACAGTCTCCAGGATCAA | 467 |
| Oy | 300 | TGTGACAGCTTCTTCAAGAACAGGGGGCATTTGTCCCTGACACTCCATGAAAGCAGGTAA | 359 |
| Dd | 468 | TGTGACAGCTTCTTCAAGAACAGGGGGCATTTGTCCCTGACACTCCATGAAAGCAGGTAA | 527 |
| Oy | 360 | CTTCTCTGTGTAACCGAAGATGTACCCCTGAGATACCCA-GGAGTTCACATG-CCGG | 417 |
| Dd | 528 | CTTCTCTGTGTAACCGAAGATGTACCCCTGAGATACCCAAGGAGTTCACATG-CCGG | 587 |

| | | | |
|-----------------------|-----------------|---|-----------------------------|
| OY | 418 | GATTATGAATGACAGCAGCTTAGTCAACATCTGTGGAAAGGTCGACGCCT | 477 |
| Db | 588 | GTATTATGAATTCACGCCACGTTAGTCAMGATCTTGAAAGAGGTGGTCAGCGTCCCT | 647 |
| OY | 478 | GTGGCAGCAAATCT | 491 |
| Db | 648 | GTTCACCAACTT | 661 |
| RESULT 5 | A1614037 | | |
| LOCUS | A1614037 | 538 bp | mRNA linear EST 21-APR-1996 |
| DEFINITION | A1614037 | Vg32f09.y1 Soares.mammary_gland NBMMG Mus musculus cDNA clone IMAGE:863081.5 similar to TR.O75144 O75144 KIAA0653 PROTEIN , mRNA sequence. | |
| ACCESSION | A1614037 | GI:4623204 | |
| VERSION | A1614037 | EST. | |
| KEYWORDS | | house mouse. | |
| SOURCE | | Mus musculus | |
| TAXIDISM | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 538) | |
| REFERENCE | | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. | |
| AUTHORS | | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index | |
| TITLE | | Unpublished (1997) | |
| JOURNAL | | Contact: Robert Strausberg, Ph.D. Email: cgapbs.r@email.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:507169 | |
| COMMENT | | This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation) Possible reversed clone: similarity on wrong strand Seq primer: -40RP from Gldco High quality sequence stop: 345. Location/Qualifiers 1..538 | |
| FEATURES | source | /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:863081" /clone_1lb="Soares_mammary_gland_NBMMG" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DHL0B" /note="Organ: mammary gland; Vector: pUT73d-Pac (pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', IGTTACCACAATCTGAAGTGGAGCGGCCGCAATGTTTTTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ., Library constructed and normalized by Benito Soares and M.Fatima Bonafido." | |
| BASE COUNT | 111 a | 135 c | 129 g 142 t 1 others |
| ORIGIN | | | |
| Query Match | 42.4% | Score 410; | DB 9; Length 538; |
| Best Local Similarity | 96.3%; | Pred. No. 8.4e-115; | |
| Matches 419; | Conservative 0; | Mismatches 16; | Indels 0; Gaps 0; |
| OY | 1 | ATGACGTAAGAAGTCCCTGTTTGTGTCTTTGGAAACAGCAGCTGTTGGAGAAG | 60 |
| Db | 104 | ATGCAGCTAAAGTGTCCCTGTTTGTCTTCCTTGGAACACAGCAGCCTGTTGGAGAAG | 163 |
| OY | 61 | CTCACATGTTTCTACGGGTTCTTTCTTGCGTCTTGCTGTTCTTGCTGCTGTGAGCAGC | 120 |

| | | | |
|----|-----|---|-----|
| Db | 164 | CTCCAGTCTTTCAGGGGTTCTTCTCGCTTGGCTCTCTCTGCTGTTGACAC | 223 |
| Qy | 121 | CTCTGTCGCTTCCTGACAGACTGAAGTCGGTGCATATGTTGGGCGACANTGGTGC | 180 |
| Db | 224 | CTCTGTGCTGCTCTCTGACAGACTGAAGTCGGTGCATATGTTGGGCGACANTGGTGC | 283 |
| Qy | 181 | AGCTGCATTGACCCGCCACGAGCGCATTTCAACTTGAAGTGGTCTGTATGTTGGCAA | 240 |
| Db | 284 | AGCTGCATTGACCCGCCACGAGCGCATTTCAACTTGAAGTGGTGTATGTTGGCAA | 343 |
| Qy | 241 | ATCGAAAACCCGAGAGTTTCGGTGACTTACTACCTGCTTACAACTCTCCAGGATCAAT | 300 |
| Db | 344 | ATCGAAAACCCGAGAGTTTCGGTGACTTACTACCTGCTTACAACTCTCCAGGATCAAT | 403 |
| Qy | 301 | GTGGACAGTTCCTCAAGAACAGGGGCCATCTGTCCCTGGACTCCATGAGAGGGTAA | 360 |
| Db | 404 | GTGGACAGTTCCTCAAGAACAGGGGCCATCTGTACCTTGAAGCTTCAATGAGAGTGGTAA | 463 |
| Qy | 361 | TTTCTCTGTGACCTGAAGATGTCAACCCCTCAGATATCCACAGAGTTCATATGCCGGTA | 420 |
| Db | 464 | TTTCTCTGTGACCTGAAGATATGTCAACCCCTCAGATATCCACAGAGTTCATATGCCGGTA | 523 |
| Qy | 421 | TTTATGATTAACGCC | 435 |
| Db | 524 | TTTATGATTAACGTC | 538 |

| | | |
|------------|---|------------------------------------|
| RESULT | | 6 |
| B637248 | | |
| LOCUS | B637248 | 577 bp mRNA linear EST 26-Oct-2001 |
| DEFINITION | B637248 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA A53060OJ13 5', mRNA sequence. | |
| ACCESSION | B637248 | |
| VERSION | B637248.1 | GI:16473033 |
| KEYWORDS | EST. | |
| SOURCE | house mouse. | |
| ORGANISM | Mus musculus | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | |
| AUTHORS | 1.(bases 1 to 577) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Komoto,H., Kouda,M., Koys,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,I., Okido,T., Saito,R., Sakai,C., Sakai,K., Sanjo,H., Sasakib., Shibata,K., Shinigawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya.T., Muramatsu,M. and Hayashizaki.Y. | |
| TITLE | RIKEN Mouse ESTs (Arakawa,T., et al. 2001) | |
| JOURNAL | Unpublished (2001) | |
| COMMENT | Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resesc.gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shihata.K., Itch ,M., Konno.H., Okazaki,Y., Muramatu.M. and Hayashizaki.Y. Normalization and subtraction of cap-trapper-selected CDNA's to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10(10), 1617-1630 (2000) waagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Obara,E., Wataliki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunra ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kirz.A. and Hayashizaki.Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10(11), 1757-1771 (2000) Konno,H., Fukushima,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki.Y. | |

D 532 GGCGCCCCACAGCCCTCCAGG---ATGAGCTACACCTTCAGCTGATCATCATTAACG 588
Q 569 GCTTACCCAGAGCCCAACCTGATTGATCAACACAGGACATAGCCTTAATAGACACG 628
D 589 GCTTACCCAGAGCCCAACCTGATTGATCAACACAGGACATAGCCTTCCTGACACG 648
Q 629 CTCTGAGAAATTAACCTGCTACTTGAACAAAGTTGGGCTCTATGATGATATCAGCAT 688
D 649 CTCTGAGAAATTAACCTGCTACTTGAACAAAGTTGGGCTCTATGATGATGATGATG 708
Q 689 TAAGGCTCCCTTGGACATCTCTGGGATGTTCTGCTGCTGATAGAAATGTGCTCTCC 748
D 709 TGAGAGTGGACGACGCCACCCAGCCTGAACATGTGCTCTGATAGAACGCTCTTCTGC 768
Q 749 ACCAAGAACTACTAGCATTAACCCAGCAGAAAGTTTCACTGGAATTAACAAAGAAC 808
D 769 AGCGAAACCTGACTGTGGGACGACAGGAATGACATCGAGAGAGACAAAGATCA 828
Q 809 CACAGAAACCCACATA 826
D 829 CAGGAATCCAGTCAGTA 846

RESULT 8
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LOCUS AA510455
DEFINITION v932f09.r1 Soares_mammary_gland_NbMWG Mus musculus cDNA clone
IMAGE:863081.5, mRNA sequence.
ACCESSION AA510455
VERSION AA510455.1 GI:2248309
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 440)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:307169
Seq primer: -28m13 rev2 ET from Amerisham
High quality sequence stop: 408.
Location/Qualifiers
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/organism="Mus musculus"
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/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia
RI: 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTACCAATCTGAACTGGAGCGCCGGAATGTTTTTTTTTTTTTTTTTTTTTTTTTTTT
T 3'1); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldou.
BASE COUNT 87 a 133 c 109 g 111 t
ORIGIN

Query Match 30.7%; Score 297; DB 9; Length 440;
Best Local Similarity 99.7%; Pred. No. 4.9e-80;
Matches 308; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Q 1 ATGAGCTAAAGTCCCTGTTTGTCTCTTGGGAACAGGACGCTGTTGGAAG 60
D 133 ATGAGCTAAAGTCCCTGTTTGTCTCTTGGGAACAGGACGCTGTTGGAAG 192
Q 61 CTCCATGTTCTAGCGGGGTTCTTCTGCTTGTGCTGCTGCTGCTGCTG 120
D 193 CTCCATGTTCTAGCGGGGTTCTTCTGCTTGTGCTGCTGCTGCTGCTG 251
Q 121 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
D 252 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Q 181 AGCTGATGACCCCGACAGCCGATTCATCTGATGATGATGATGATG 240
D 312 AGCTGATGACCCCGACAGCCGATTCATCTGATGATGATGATGATG 371
Q 241 ATGGAAGCCAGAAAGTTGGGCTGCTTACTGCTGCTTCAAGTCCAGGATCAAT 300
D 372 ATGGAAGCCAGAAAGTTGGGCTGCTTACTGCTGCTTCAAGTCCAGGATCAAT 431
Q 301 GTGACAGCT 309
D 432 GTGACAGCT 440

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:307169
Seq primer: -28m13 rev2 ET from Amerisham
High quality sequence stop: 408.
Location/Qualifiers
1..440
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="Soares_mammary_gland_NbMWG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia
RI: 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTACCAATCTGAACTGGAGCGCCGGAATGTTTTTTTTTTTTTTTTTTTTTTTTTTTT
T 3'1); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into

FEATURES
source
1..1083
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:575883"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo

BM923293 1083 bp mRNA linear EST 12-MAR-2002
LOCUS BM923293
DEFINITION AGENCOURT_6625900 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:575883
5', mRNA sequence.
ACCESSION BM923293
VERSION BM923293.1 GI:19373672
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1083)
NIH-MGC <http://mgi.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM12803 row: 9 column: 12
High quality sequence stop: 741.
Location/Qualifiers
1..1083
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/db_xref="taxon:9606"
/clone="IMAGE:575883"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo

| | | | | |
|-----------------------|--------|--------------------|--------|-------------|
| Query Match | 22.7%; | Score 219; | DB 13; | Length 816; |
| Best Local Similarity | 65.9%; | Pred. No. 7.1e-56; | | |

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: aslimpso@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.luigiw.org.br/scripts/gethtml2.pl?tl=PM2&t2=DM2-CT0238>) (290999-001.g01&t3=1999-09-29&t4=1)

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DEFINITION   yj34c12.r1 Soares Infant brain IN1B Homo sapiens cDNA clone
IMAGE:34465 5', mRNA sequence.
ACCESSION   R23544
VERSION     R23544.1
KEYWORDS    EST.
SOURCE      Homo sapiens
ORGANISM    human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 422)
AUTHORS     Hillier,L., Clark,N., Duboue,T., Ellison,K., Hawkins,M., Holman
            M., Hultman,M., Kucab,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treaskis,E., Waterston
            R., Williamson,A., Wohlmann,P. and Wilson,R.
            The Mashu-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.wustl.edu
            Insert Size: 2783
            High quality sequence stops: 364
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
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            Seq primer: M13Rpl
            High quality sequence stop: 364.
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                1..422
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                   /db_xref="taxon:9606"
                   /clone="IMAGE:34465"
                   /clone_lib="Soares Infant brain IN1B"
                   /sex="female"
                   /dev_stage="73 days post natal"
                   /lab_host="DH10B (ampicillin resistant)"
                   /note="Organ: whole brain; Vector: Lambda BA; Site:1: Not
            I; Site:2: Hind III; 1st strand cDNA was primed with a Not
            I - oligo(dT) primer [5';
            AACGGAGAGATTGGCGCCCGCCAGAGATTTTATTTT 3'];
            double-stranded cDNA was ligated to Hind III adaptors
            (Pharmacia), digested with Not I and directionally cloned
            into the Not I and Hind III sites of the Lambda BA vector.
            Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bernaldo."
            constructed by Bento Soares and M.Fatima Bernaldo."
FEATURES
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    100 a 122 c 121 g 78 t 1 others
    Query Match 15.7%; Score 151.6; DB 14; Length 422;
    Best Local Similarity 67.3%; Pred. No. 3e-35;
    Matches 230; Conservative 0; Mismatches 109; Indels 3; Gaps 1;
    485 CAACCTGAGTACACCTGTATCATGACACCTGTGATAGTCCAACCCGGGCGCAGAACGTA 544
    1 CAAACTGACGCGCGCCGTCGTCACGCGCCGCCACCGCCCGCCCGCAGG--ATGAGCTCA 57
    545 CCTAACCTGCAATGCCAAGATGGCTACCCAGAGCCCAACTGTATTGGATCAACACAA 604
    58 CTTTACAGTGATCAATCAATTAAGCGGCTACCCAGGCGCCAAAGCTGTACGTGATCAATAGA 117
    605 CGGACATAGACCTTATTAACACGGGCTGCGAGATTAACACTGTACTGTGACATAGTTGG 664
    118 CGGACAAACAGCCTGCTGGACAGCGCTGTGCGAATAGACACCGCTTTTGTGAACATCGGG 177
    665 GCGCTGTATGATTAATCAGACACATTAAAGGCTCCCTTGGACATCTCGTGGGGATGTTCTGT 724
    178 GCTTATATGACGTGCTGACGCGTGTGAGATGCGACGAGCCCGCGGATGATTTGGCT 237
    725 GCTGCTAGAGAAATGGCTCTCCACCGAGACATCTACTAGCATTTTGCCAGGCGAGAAATT 784

```

| | | | |
|---|--|---|-----|
| Db | 238 | GCTGCATAGACGACTGGTTCCTTGCAK6CAGAACCCTACTGTGGCAGGCCAACAAGGAATG | 297 |
| QY | 785 | TCACGTGAATAAACAAAGAACCCACAGAGAAACCCACAAAATA | 826 |
| | | | |
| Db | 298 | ACATCGAGAGAGAGACAAAGATCACAGAGAAATCCAGTCAAGTA | 329 |
| RESULT 15 | | | |
| Bf776710 | | | |
| LOCUS | | | |
| DEFINITION | 287583 MARC 3BOV Bos taurus cDNA 5', mRNA sequence. | | |
| ACCESSION | Bf776710 | | |
| VERSION | Bf776710.1 GI:12124610 | | |
| KEYWORDS | EST. | | |
| SOURCE | Cow. | | |
| ORGANISM | Bos taurus | | |
| | Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; | | |
| | Bovidae; Bovinae; Bos. | | |
| REFERENCE | 1 (bases 1 to 476) | | |
| AUTHORS | Smith,T.P.L., Grosses,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett, G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G., Pettea,G., Holt,I., Karameycheva,S., Liang,F., Queckenbush,U. and Keefe,J.W. Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle | | |
| TITLE | Genome Res. 11 (4), 626-630 (2001) | | |
| JOURNAL | 21180013 | | |
| MEDLINE | Contact: Smith TPL | | |
| COMMENT | USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smithemail.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -minmatch 12 options. PCR Primers FORWARD: AGGAACAGCATATGACCAT BACKWARD: GTTTCCAGTAGTCACGACG Plate: 92 row: J column: 22 Seq primer: ATTAGGTACACTATTAC. Location/Qualifiers 1..476 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC 3BOV" /tissue_type="pooled" /lab_host="DHL0B" /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle." | | |
| BASE COUNT | 111 a 139 c 141 g 85 t | | |
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| Query Match | 15.2%; Score 147.2; DB 12; Length 476; | | |
| Best Local Similarity | 66.4%; Pred. No. 7.1e-34; | | |
| Matches 247; Conservative 0; Mismatches 113; Indels 12; Gaps 2; | | | |
| QY | 454 TTGGAAGAGGTGGTCAGGCTGGCTGTGGCAGCAAACCTTCAGTACACCTGTATCAGCAC | 513 | |
| | | | |
| DB | 23 TTGGAAGTTGGCGTCACGCTGCAGCTGGCAGCAAACCTACAGACATCCGTGTGACGC | - 80 | |
| QY | 514 TCTGATAGCTCCAAACCGGGCCAGGACGATCTACACCTGCATGTCCAAGAATGGCTAC | 573 | |
| | | | |
| DB | 81 -----GCCCTCCACAGAGACGAGAGCTCAACCTTCACAGCTGACGCTACCAACGGCTAC | 133 | |
| QY | 574 CCAGAGCCCACACCTGATTTGGATCAACAACAGGGCAATAGCGTAATTGACACGGCTGTG | 633 | |
| | | | |
| DB | 134 CCGGCGCAAAATGTGTACTGATGCATACAAAGAGGCAACAGCGTGTGACAGCGCCCTTG | 193 | |

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QY 209 TCACCTTGAGTGTGTATGTATGTATTTGGCAATTCGAAACCCAGAAAGTTCCGTACTT 268
Db 262 TTGATTTAAATGATGTTTACGTATATTGGCAACAGTGTGAAACCCGTTGAGTACTT 321
QY 269 ACTACTGCTCTTCAAGTCTCCAGGATCAATGTGACATCTCTCAAGAAACAGGGGCC 328
Db 322 ACACATCCACAGAACAGTCTCTTGAAACAGTGGACACCCGCTACCCGAAACCGAGGCC 381
QY 329 ATCTGTCCCTGAGCTCAGTAAAGAGGTAATCTCTCTGTATCTGTAAGATGTACACC 388
Db 382 TGATGTACCGGCGGATCTCTGCGGCGACATCTCTCCCTGTGTTCACGTACGCC 441
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Db 442 CCGAGGACGAGCAAGATTTACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 498
QY 449 AGATCTTGAAGAGTGTGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 508
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QY 509 GCACCTGTGATAGTCCAAACCCGGCCAGAGAGTACTTACCTGATGTCCAAAGATG 568
Db 559 GCGCCCCCAGACGCTCCAGG--ATGAGCTCACCTTCACGTGTATCATCATATAAG 615
QY 569 GCTACCCAGAGCCAACTGTTATGATCAACAAACGAGCAATAGCCTAATAGACAGG 628
Db 616 GCTACCCAGAGCCAACTGTTATGATCAACAAACGAGCAATAGCCTGCTGAGCAGG 675
QY 629 CTCTGCAATTAACACTGTCTACTTGAACAAGTTGGGCTGTATGATGTAATACACAT 688
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QY 689 TAAGGCTCCCTTGACATCTGCGGGGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
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QY 749 ACCAGAACATCACTAGCATAGCCAGGACAGAAAGTTTCACTGGAATTAACAAAGAAC 808
Db 796 AGCAGAACCTGACTGTGCGAGCAGACAGAAATGACATCGAGAGAGACAGATCA 855
QY 809 CACAGGAACCCACATA 826
Db 856 CAGAGATCCAGTCAGTA 873

RESULT 2
Sequence 64, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: P2043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 64
LENGTH: 2751
TYPE: DNA
ORGANISM: Homo sapiens
US-09-789-561-64

Query Match 31.0%; Score 299.2; DB 10; Length 2751;
Best Local Similarity 64.6%; Pred. No. 7.5e-85;

Matches 477; Conservative 1; Mismatches 254; Indels 6; Gaps 2;
QY 89 GTCCTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
Db 231 GTCCTGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 290
QY 149 TCGGTCAATGTTGGGCAATGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
Db 291 TCAGAGGATGTAGGAGGAGGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 350
QY 209 TCACCTTGAGTGTGTATGTATGTATTTGGCAATTCGAAACCCAGAAAGTTCCGTACTT 268
Db 351 TTGATTTAAATGATGTTTACGTATATTGGCAACAGTGTGAAACCCGTTGAGTACTT 410
QY 269 ACTACTGCTCTTCAAGTCTCCAGGATCAATGTGACATCTCTCAAGAAACAGGGGCC 328
Db 411 ACCACATCCACAGAACAGTCTCTTGAAACAGTGGACACCCGCTACCCGAAACCGAGGCC 470
QY 329 ATCTGTCCCTGAGCTCCATGAGAGGTAATCTTCTCTGTATCTGTAAGATGTACACC 388
Db 471 TGATGTACCGGCGGATCTCTGCGGCGACATCTCTCCCTGTGTTCACGTACGCC 530
QY 389 CTGAGATATACCGAGGATTCACATGCCGGTATTTATGATACAGCCACAGATTAGTCA 448
Db 531 CCGAGGACGAGCAAGATTTACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 587
QY 449 AGATCTTGAAGAGTGTGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 608
Db 588 AGGTTTGTAGCTTTGAGGTTACACTGTGATGTGAGCAAACTTCAGCGTCCGCTGTCA 647
QY 509 GCACCTGTGATAGTCCAAACCCGGCCAGAGAGTACTTACCTGATGTCCAAAGATG 568
Db 648 GCGCCCCCAGACGCTCCAGG--ATGAGCTCACCTTCACGTGTATCATCATATAAG 704
QY 569 GCTACCCAGAGCCAACTGTTATGATCAACAAACGAGCAATAGCCTAATAGACAGG 628
Db 705 GCTACCCAGAGCCAACTGTTATGATCAACAAACGAGCAATAGCCTGCTGAGCAGG 764
QY 629 CTCTGCAATTAACACTGTCTACTTGAACAAGTTGGGCTGTATGATGTAATACACAT 688
Db 765 CTCTGCAATTAACACTGTCTACTTGAACAAGTTGGGCTGTATGATGTAATACACAT 824
QY 689 TAAGGCTCCCTTGACATCTGCGGGGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
Db 825 TGAGGATCGACGAGCCCGAGCGTGAACATTTGGCTGTCTCATAGAACGCTTCTGTC 884
QY 749 ACCAGAACATCACTAGCATAGCCAGGACAGAAAGTTTCACTGGAATTAACAAAGAAC 808
Db 885 AGCAGAACCTGACTGTGCGAGCAGACAGAAATGACATCGAGAGAGACAGATCA 944
QY 809 CACAGGAACCCACATA 826
Db 945 CAGAGATCCAGTCAGTA 962

RESULT 3
US-09-764-853-210
Sequence 210, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, proteins, and antibodies
FILE REFERENCE: F0206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 210
LENGTH: 2616
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-853-210

PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1655
LENGTH: 1879
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1_N17300
US-09-917-800A-1655

Query Match 3.5%; Score 33.4; DB 10; Length 1879;
Best Local Similarity 51.7%; Pred. No. 2.3;
Matches 76; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

OY 504 CATTGACGCTGATGATGCTCAACCGGGCGAGGAGTACCTGACCTGATGCTCA 563
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 726 CACCAAGCTCTCCAAACAAAGTCAATGACCCCTGGAAAGGACCTTCTCGGAGCGAGAA 667
OY 564 GAATGCTACCCAGAGCCCAACCTGATGTGATCAACACAGGACAATAGCCCTAATAGA 623
|| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
DB 666 ACAGGCTCCCGGATTCGGGCTTCTTACATGATGATCTAGTACACACAGGTCCTATAT 607
OY 624 CAGGCTCTGCAAGATTAACACTGTCTA 650
|| || || || || || || || || || || || || || || || || || || || || || || || || ||
DB 606 ACCACCTTTCAGAAATGACTATCCA 580

RESULT 8

US-09-783-590-61/c
Sequence 61, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Haseltine, Patrick J.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16,2C1
CURRENT APPLICATION NUMBER: US/09/783,590
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 236
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (11)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (130)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (135)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (191)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (200)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (201)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-61

Query Match 3.4%; Score 33.2; DB 10; Length 236;
Best Local Similarity 61.7%; Pred. No. 0.78;
Matches 50; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 756 CATCTAGCATTTAGCCAGAGAGTTTCACTGGAATTAACAAAGAACCCACAGCA 815
|| || || || || || || || || || || || || || || || || || || || || || || || || ||
DB 219 CCTCAACATCATTTAGTCANNAGGAAATNCAAAATTAATAATTACAGTAATTACCTCTACA 160
OY 816 ACCCCACAATAATGAGTTAAA 836
|| || || || || || || || || || || || || || || || || || || || || || || || || ||
DB 159 AATCTATAGATGAGTTAAA 139

RESULT 9

US-09-960-352-15003
Sequence 15003, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 15003
LENGTH: 229
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: unsure
LOCATION: (63)...(64)...(67)...(69)...(70)...(96)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 64-LIB3058-040-Q1-K1-H8
US-09-960-352-15003

Query Match 3.4%; Score 33; DB 10; Length 229;
Best Local Similarity 60.0%; Pred. No. 0.88;
Matches 54; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 752 AGAATCATCTAGCATGAGCCAGAGAAAGTTCACTGGAATTAACAAAGAACCCAC 811
|| || || || || || || || || || || || || || || || || || || || || || || || || ||
DB 94 AGNAAAAACCAAGATTTAGCAGAAATTAATAAACTTGAATTAACCAAAAACCAAA 153
OY 812 AGGAACCCACAAATAATGAGTTAAAGTCC 841
|| || || || || || || || || || || || || || || || || || || || || || || || || ||
DB 154 ACAGAAAGGAAAAAAGCAAGCAAGCC 183

RESULT 10

US-09-960-352-9888/c
Sequence 9888, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.

```

: APPLICANT: Tao, Nengping
: APPLICANT: Byatt, John C.
: APPLICANT: Mathialagan, Nagappan
: TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
: TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
: FILE REFERENCE: 16511.006/37-21.10298/C
: CURRENT APPLICATION NUMBER: US/09/960,352
: CURRENT FILING DATE: 2001-09-24
: NUMBER OF SEQ ID NOS: 15112
: SEQ ID NO 9888
: LENGTH: 425
: TYPE: DNA
: ORGANISM: Bos taurus
: OTHER INFORMATION: Clone ID: 42-LIB34-082-Q1-E1-C6
: US-09-960-352-9888

```

| | | | | |
|-----------------------|-----------------|----------------|-----------|-------------|
| Query Match | 3.48; | Score 33; | DB 10; | Length 425; |
| Best Local Similarity | 58.8%; | Pred. No. 1.3; | | |
| Matches 57; | Conservative 0; | Mismatches 40; | Indels 0; | Gaps 0 |

Db

```
516 TGATAGCTCCAAACCGGGGCCGAGAACGTACTTACCTTGTCATGTCCAAGAATTGGCTACCC 575
||||| |||| | ||||||| ||||| ||||| ||||| |||||
301 TGAATGCTGCACGCTTTCAACCAGGAACGTGTTCCAGGCCCAACAGGCCACACAATTGTTGCCAC 2422
```

Qy 576 AGAGCCCAACCGTATTGGATCAACACACAGGACAT 612
| | | | | | | | | | | | | | | | | |
Db 241 AAGGCACATCCGATGGGCTCCACAGTAACGCCCAT 205

RESULT 11
US-09-820-905-3

```

; Sequence 3, Application US/09820905
; Patent No. US20020142938A1
; GENERAL INFORMATION:

```

1 TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
2
3 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
4
5 TITLE OF INVENTION: AND USES THEREOF

;; CURRENT APPLICATION NUMBER: US/09/820,905
: CURRENT FILING DATE: 2001-03-30

```
; NUMBER OF SEQ ID NOS: 5
;
; SOFTWARE: FastSeq for Windows Version 4.0.0
```

```

; SEQ ID NO 3
;
; LENGTH: 203654
;

```

TYPE: DNA
ORGANISM: HUMAN

NAME/KEY: misc_feature
LOCATION: (1) .. (203654)

OTHER INFORMATION: n = A, T, C or G
US-09-820-905-3

| | | | | |
|-----------------------|--------|---------------|--------|----------------|
| Query Match | 3.48; | Score 33; | DB 10; | Length 203654; |
| Best Local Similarity | 50.38; | Pred. No. 52; | | |
| Matches | 81; | Mismatches | 80; | Indels 0; |

Qy 682 AGCACATTAAAGGCTCCCTTGGAATCTGTGGGATGTTCTGTGCCTAGACAATGTG 741
| | | | | | | | | | | | | |
Db 67304 AGAAGTAGTGGCTTAAGAAGTAGACCTCAGACAGAGGGGTTCGATTTCGTAGAACCAg 67363

Oy 742 GCCTCCACCAGAACATCATTGACATTAGCCAGGCAGAAAGTTTCACTGGAAATAACACA 801

Db 67364 GCTACACAGCAGAGGTGAACAGCAGCAGCCACAGCAGAAGCTTCATCTATATTACAGC 674

| | | | |
|----|-------|--|-------|
| OY | 802 | AAGAACCCACAGGAAACCCACATAATGAGTTAAAGTCCT | 842 |
| | | | |
| Db | 67424 | CACCTCCCCACTGCTCACATAACCACTGAGCTCCGCCCTCCT | 67464 |

RESULT 12
US-09-884-441-346/c
; Sequence 346, Application US/09884441

```

: Patent No. US20020119158A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Algate, Paul A.
:
: APPLICANT: Carter, Darlick
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
:
: TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
:
: FILE REFERENCE: 210121.462C7
:
: CURRENT APPLICATION NUMBER: US/09/884,441
:
: CURRENT FILING DATE: 2001-06-18
:
: NUMBER OF SEQ ID NOS: 489
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 346
:
: LENGTH: 370
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-884-441-346

```

| | | | | |
|-----------------------|-----------------|----------------|-----------|-------------|
| Query Match | 3.48; | Score 32.6; | DB 10; | Length 370; |
| Best Local Similarity | 57.38; | Pred. No. 1.6; | | |
| Matches 59; | Conservative 0; | Mismatches 44; | Indels 0; | Gaps 0; |

Oy 368 TGIACCTGAAGCATGTCAACCCCTCAGGATACCAGGAGTTTCACATGCCGGGATTTTATGA 427
+
Db 263 TTCTACTGCCTTATGTCAACCAACGACCTATCAGGAGCACCTTCACAGACCTGATGA 204

OY 428 ATACAGCCACAGAGTTAGTCAAGATCTTGGAAGAGGTGTCAG 470
 ||| || | | | | | | | | |
Db 203 ATAGCAACAGCAATTTCGGGAGGCTTTGGAGAAGCTGGAGAG 161

RESULT 13
US-09-764-860-799

Patent No. US20020094953A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.

```

; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17

```

; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0.6

```

; SEQ ID NO 799
; LENGTH: 32188

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```

; TYPE: DNA
; ORGANISM: Homo sapiens

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Query Match

| | | | | | | | | | |
|---------|---|--------------|----|------------|-----|--------|----|------|----|
| Matches | 83; | Conservative | 0; | Mismatches | 84; | Indels | 0; | Gaps | 0; |
| 363 | CTCTCTGACCTGAGAGATGTCAACCCCTTCAGATACCCAGAGACTTCACATGCGCGGATTT | 422 | | | | | | | |

Db 3949 CTCCTGGGTCACAGTATCTTCCTGCTCAGCCTCCCGAGTACCTGGGATTACAGGCATG 4008
QY 423 TATGATACAGCCACAGAGTTAGTACAGATCTTTGGAAAGAGTGTGAGGCTGCGTGTGGC 482

Db 4009 CACCACCAACCCAGCTAGTTTGTATTTTATAGTAGAGATGGGGTTTCTCCAAGTTGGTC 4066
QY 483 AGCAAACTTCAGTACACCTGTTCATTCAGCACCTCTGATAGTCCAACC 529

Db 4069 AGGCTGGTCTCGTACTCCTGACTCAGGTTATCTGCCCCGCTCGGC 4115

RESULT 14
US-09-910-174A-22
; Sequence 22, Application US/09910174A
; Patent No. US20020106730A1
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.


```
US-09-105-058C-26/C
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blahar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; TYPE: DNA
; LENGTH: 2565
; ORGANISM: Homo sapiens
; US-09-105-058C-26

Query Match
Best Local Similarity 52.5%; Pred. No. 1.9; Length 2565;
Matches 95; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 281 ACAAGTCTCCAGGATCATGTGACAGTTCCTACAGAACAGGGCCATCTCCCTGG 340
DB 457 ACTCGGCTCCAAAGATGAATAAGCAATGTCTCCAGTAACAGAACCA-GTCTCCGAG 399
QY 341 ACTCCATGAAGCAGGGTACTTCTCTGTGTAAGATGTCACCCCTCAGATACCC 400
DB 398 ACAGTCTCATCTCTTGATGTGTGACAGACAGCCAGATTCAGACCCAGACATC 339
QY 401 AGGAGTTCACATGCCGGTATTATGAATACAGCCACAGATGATGCAAGATCTGGAG 460
DB 338 AGGAACACCAACCGGTGTAAGACAGCCGCCAGCCCCGGGTCTCTCCAGGGGTGTAG 279
QY 461 A 461
DB 278 A 278

RESULT 3
US-09-177-650-6/C
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; TYPE: DNA
; LENGTH: 2914
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
```

```
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
; US-09-177-650-6

Query Match
Best Local Similarity 52.5%; Pred. No. 2.1; Length 2914;
Matches 95; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 281 ACAAGTCTCCAGGATCATGTGACAGTTCCTACAGAACAGGGCCATCTGTCTGG 340
DB 529 ACTCGGCTCCAAAGATGAATAAGCAATGTCTCCAGTAACAGAACCA-GTCTCCGAG 471
QY 341 ACTCCATGAAGCAGGGTACTTCTCTGTGTAAGATGTCACCCCTCAGATACCC 400
DB 470 ACAGTCTCATCTCTTGATGTGTGACAGACCCAGATTCAGACCCAGACATC 411
QY 401 AGGAGTTCACATGCCGGTATTATGAATACAGCCACAGATGATGCAAGATCTGGAG 460
DB 410 AGGAACACCAACCGGTGTAAGACAGCCGCCAGCCCCGGGTCTCTCCAGGGGTGTAG 351
QY 461 A 461
DB 350 A 350

RESULT 4
US-09-404-879A-346/C
; Sequence 346, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; TYPE: DNA
; LENGTH: 370
; ORGANISM: Homo sapiens
; US-09-404-879A-346

Query Match
Best Local Similarity 57.3%; Pred. No. 0.96; Length 370;
Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 368 TGTAAGTGAAGATGTACCCCTCAGGATACCCAGGATTCACATGCCGGTATTATGA 427
```

DB 263 TCTACTGCTTATGTCACCAACGACCTATCAGAGGACCTCCAGAGCCGTGATGA 204
QY 428 ATACAGCCACAGATTACTCAAGATCTTGAAGAGGTGCTGAC 470
DB 203 ATAGCAACAGCAATTTCGGGAGGCTGTGAGAAAGCTGAGAG 161

RESULT 5

US-08-545-809A-2
Sequence 2, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: GM1
US-08-545-809A-2

Query Match 3.4%; Score 32.6; DB 3; Length 512;
Best Local Similarity 47.7%; Pred. No. 1.1; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 278 CTTACAGTCTCAGGAGTCAATGTGACAGTCTCTACAGAGAGGGCCATCTGCTCC 337
DB 224 CCGTCAAGGCTTGTGATACCTTCACCGGCTACTATATGACCTGGTGCAGACAGGCC 283
QY 338 TGGACATCCATGAAGCAGGGAATCTCTCTGTACTGAAAGATGTCACCCCTCAGAGATA 397
DB 284 CTGGACAAGGGCTTGAAGTGGATGGATGATCAACCCCTAAGTGTGTCACAAACTATG 343
QY 398 CCCAGAGTTTACATCCCGGATTTATGATATACAGCCACAGAGATAGTACAGATCTTG 457
DB 344 CACAGAAAGTTTACGGGCGACAGGTACCATACACAGGACACGTCATCAGCAGCCTTACA 403

QY 458 AAGAGTGTGACGCTGCG 476
DB 404 TGGAGCTGACAGAGCTGAG 422

RESULT 6

US-08-017-570-3
Sequence 3, Application US/08017570
Patent No. 5472693
GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570
FILING DATE: 19930216
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: 1..373
US-08-017-570-3

Query Match 3.3%; Score 32.2; DB 1; Length 373;
Best Local Similarity 47.3%; Pred. No. 1.3; Indels 0; Gaps 0;

Matches 97; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 270 CTACCTGCTTCAAGTCTCCAGGATCATGTGACAGATTCTTACAGAGAGGGGCCA 329
DB 54 CAAAGATGCTCCACAGAGCTTGTGCTTCAACATTAAGACTATATGCACTGGGTGAA 113
QY 330 TCTGTCCCTGGACTCATGAGACAGAGGTAATCTCTCTGTACTGGAAGATGTCACCC 389
DB 114 GCAGAGGCTGTGAACAGGGCTGTGAGTGGATGGATGATGCTGAGAAATGTGATAC 173
QY 390 TCAGGATACCCAGAGATCACATGCGGGTATTTATGATACAGCCACAGAGTTAGTAA 449
DB 174 TGAATATGCCCCGAAGTTCAGAGGCAAGCCACTATGACTACAGACATCTCCCAACAC 233
QY 450 GATCTTGAAGAGGTGTGACAGCTG 474
DB 234 AGCTTACTGACAGCTCAGCAGCTG 258

CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..373
PCT-US94-01709-5

Query Match 3.3%; Score 32.2; DB 5; Length 373;
Best Local Similarity 47.3%; Pred. No. 1.3;
Matches 97; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 270 CTACCGCTTACAGTCTCCAGGAGTATGAGACAGTCTCTACAGAGAGGGGCCA 329
DB 54 CAGAGATGCTCTGACAGCTTCTGCTCAACATTAAAGACTATATGACATGGGGA 113
QY 330 TCTGTCCCTGAGACTCCATGAGCAGGGTAACTTCTCTGTACTGTAAGATGTCACCC 389
DB 114 GCAGAGGCTGAGAACAGAGGCTGAGATGATGATGATGATGATGATGATGATGATG 173
QY 390 TCAGGATACCCAGAGATTCAATGCGGGATTTATGATGATGATGATGATGATGATG 449
DB 174 TGAATATGCCCCAGAGTTCAGGGCAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 233
QY 450 GATCTGGAAGAGTGTGTCAGGCTG 474
DB 234 AGCTTACCTGACGCTCAGCAGCCTG 258

RESULT 12
US-08-188-228-47
Sequence 47, Application US/08188228
Patent No. 559725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 3048 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-188-228-47

Query Match 3.3%; Score 32.2; DB 1; Length 3048;
Best Local Similarity 48.1%; Pred. No. 3.8;
Matches 91; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 571 TACCCAGAGCCCACTGATTTGATCAACACAGGACATATGCTTATAGACAGCGCT 630
DB 2052 TACCTAGAGGCCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 2111
QY 631 CTCCAGATATACCTGCTACTGATGACAGAGTGGGCTGATGATGATGATGATGATG 690
DB 2112 CTGTCCACACGCTCATATCAAAAGTCAAGTGTGCTCATGTATATACAGGGGACTGC 2171
QY 691 AGGCTCCCTTGACATCTGCTGGGATGTTCTGTGCTGCTGATAGAGATGTGCTCTCAC 750
DB 2172 ACCACATTTGGCCCATGAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2231
QY 751 CAGACATC 759
DB 2232 ATCTGATC 2240

RESULT 13
US-08-332-643-41
Sequence 41, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEX: (312) 984-9740
FAX: 25-3856
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 3048 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-332-643-41

Best Match
Best Local Similarity 3.3%; Score 32.2; DB 1; Length 3048;
Matches 91; Conservative 0; Mismatches 98; Indels 0; Gaps 0.

QY 571 TACCCAGAGGCCAACCTTATGATCAACAAGCAGCAATAAGCTTAAGACAGGCT 630
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2052 TACCTGGAGGCGGGGTGATGAGCTGCCCATCATGTCACAGACTGTGGAACCTCCC 2111
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 631 CTGCAGAAATACACTGTCTACTTGGAACAAGTTGGCCCTGTATGATGTAATCAGCACATTA 690
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Db 2112 CTGTCCAACACGCTCATCATCAAAGTCAAAGGTGTGCCATGTGACACAMCGGAGACTGC 2171
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 691 AGGCTCCCTTGGAATCTCGTGGGATGTTCTGTGCTGCTAGAGAATGTGCTCTCCAC 750
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2172 AOCACATTGGGCGACGTGCAGCGSGCTGTGGCACC GGTCATGTCATCTGCATCTCTC 2231
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QY 751 CAGAACATC 759
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Db 2232 ATCTGCATC 2240

RESULT 14
US-08-332-638-47
Sequence 47, Application us/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:

```

: NAME: NO. 5646250and, Greta E
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31340
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-0448
: TELEFAX: 25-3856
: TELEPHONE: (312) 474-6300
: INFORMATION FOR SEQ ID NO: 47:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3048 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-332-638-47

Query Match          3.3%; Score 32.2; DB 1; Length 3048;
Best Local Similarity 48.1%; Pred. No. 3.8;
Matches 91; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 571 TACCAGAGCCCCAACCTGATTTGGATTCAGACACACGAGCAATAGCCTATATAGACAGCGCT 630
DB 2052 TTACTTGGAGAGCCGGGATGATGACGTCCTCCCATCATGCTCAGACACTCTGGAAACCTCC 2111
QY 631 CTGCAGATATACACTGCTCTACTTGAACAAGTTGGCCCTGTATGATGTAATCAGACATTA 690
DB 2112 CTGTCAACACGCTCATCATCAAAAGTCAAGAGTGTGCCCATGTGATGATGACAAAGGGGACCTG 2171
QY 691 AGGCTCCCTGGACATCTGTGGGAGATGTTCTGTGCTGCGTGAAGANTTGGCTCTCCAC 750
DB 2172 ACCACATTGGGGCAGGTGGACCGGCTGGTCTGGGACCGGTGCCATCTGTGCGCATCTTC 2231
QY 751 CAGAACATC 759
DB 2232 ATCTGCATC 2240

RESULT 15
5169760-3
: PATENT NO. 5169760
: APPLICANT: WILCON, EDWARD R.
: TITLE OF INVENTION: METHOD, VECTORS AND HOST CELLS FOR
: THE CONTROL OF EXPRESSION OF HETEROLOGOUS GENES FROM LAC
: OPERATED PROMOTERS
: NUMBER OF SEQUENCES: 3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/386,821
: FILING DATE: 27-JUL-1989
: SEQ ID NO:3
: LENGTH: 7366
5169760-3

Query Match          3.3%; Score 31.4; DB 6; Length 7366;
Best Local Similarity 52.7%; Pred. No. 11;
Matches 68; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 45 GCCCTGTTGGAGAAGAGCTCCAGTGTTCAGCGGGTCTTTCTGTGCTGTGCTGTTCTT 104
DB 5152 GCGATGGTGGGAAAAAGCGCCCTGCTGGTGGCGACATATATGTCTGTAGCTATATATG 5211
QY 105 GGTGCTGTTGAGACACCTCTGTGCTGCTCTCTGACAGACTCAAGTCGGTGCATATGTGG 164
DB 5212 GCTCATCGTTCGCCACCTCAGCGCTGGAAGTGTTATTTCTGAAAGCGCTGATATGTTTG 5271
QY 165 CAGCAATGT 173
DB 5272 AAGTACCGT 5280

Search completed: November 17, 2002, 05:28:28
Job time : 62.118 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 01:43:50 ; Search time 160.997 Seconds

(without alignments)
12085.504 Million cell updates/sec

Title: US-09-728-421D-11
Perfect score: 864

Sequence: 1 atgcgctggcagtcctg.....tccaacagctatgcaagt 864

scoring table: IDENTITY_NDC

GAPOB 10.0 , GAPEX 1.0

Searched: 2185239 seqs, 1125999159 residues

| T | number of hits satisfying chosen parameters: | 4370478 |
|---|--|---------|
| 1 | number of hits satisfying chosen parameters: | 4370478 |

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 s

Listing first 45 summaries

Listing first 45 summaries

Database

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| 9 | /SID52/gcgdata/genseq/genseqn-emb1/NA1988.DAT * |
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| 22 | /SID52/gcgdata/genseq/genseqn-emb1/NA2001.DAT * |
| 23 | /SID52/gcgdata/genseq/genseqn-emb1/NA2002.DAT * |
| 24 | /SID52/gcgdata/genseq/genseqn-emb1/NA2002.DAT * |

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Score | Query Match | Length | DB | ID | Description |
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| 1 | 864 | 100.0 | 864 | 21 | AAAG4556 | DNA sequence encode |
| 2 | 864 | 100.0 | 864 | 24 | ABK87593 | CDNA encoding human |
| 3 | 864 | 100.0 | 906 | 22 | AAH77869 | Nucleotide sequenc |
| 4 | 864 | 100.0 | 953 | 22 | AAF79921 | Nucleotide sequenc |
| 5 | 864 | 100.0 | 1294 | 21 | AAAG4557 | DNA sequence encod |
| 6 | 864 | 100.0 | 1294 | 24 | ABK87594 | CDNA encoding human |
| 7 | 864 | 100.0 | 1453 | 22 | AAH77870 | Nucleotide sequenc |
| 8 | 864 | 100.0 | 1548 | 22 | AAH00423 | Human B7-3 CDNA. |
| 9 | 863.6 | 100.0 | 2114 | 22 | ABA06726 | Human CDNA SEQ ID |

| | | | | | | | |
|----|----|-------|-------|-------|-------|------|----------|
| 45 | 10 | 863.6 | 100.0 | 2.751 | 2.214 | 2.22 | AAB28855 |
| 44 | 11 | 863.6 | 100.0 | 2.751 | 2.214 | 2.22 | AAE91981 |
| 43 | 12 | 862.4 | 99.8 | 2.616 | 2.214 | 2.22 | ABA05544 |
| 42 | 13 | 862.4 | 99.8 | 2.616 | 2.214 | 2.22 | ABA05722 |
| 41 | 14 | 862.4 | 99.8 | 2.622 | 2.214 | 2.22 | ABA28885 |
| 40 | 15 | 862.4 | 99.8 | 2.751 | 2.214 | 2.22 | AAAS2479 |
| 39 | 16 | 716 | 82.9 | 7.16 | 2.214 | 2.22 | AA500442 |
| 38 | 17 | 699.8 | 81.0 | 1.331 | 2.214 | 2.22 | AAE79933 |
| 37 | 18 | 338 | 39.1 | 4.60 | 2.214 | 2.22 | AAE79933 |
| 36 | 19 | 289.6 | 34.7 | 5.66 | 2.214 | 2.22 | AAA64555 |
| 35 | 20 | 299.6 | 34.7 | 9.96 | 2.214 | 2.22 | AAE87599 |
| 34 | 21 | 299.6 | 34.7 | 2.718 | 2.214 | 2.22 | AAE79933 |
| 33 | 22 | 298.4 | 34.5 | 2.729 | 2.214 | 2.22 | ABL35022 |
| 32 | 23 | 277.8 | 32.2 | 1.759 | 2.214 | 2.22 | AAE79933 |
| 31 | 24 | 277.8 | 32.2 | 1.830 | 2.214 | 2.22 | AAE79933 |
| 30 | 25 | 144.6 | 16.7 | 5.45 | 2.214 | 2.22 | AAA43833 |
| 29 | 26 | 126.2 | 14.6 | 8.26 | 2.214 | 2.22 | ABA05722 |
| 28 | 27 | 126.2 | 14.6 | 8.26 | 2.214 | 2.22 | ABA28855 |
| 27 | 28 | 60 | 6.9 | 2.685 | 2.214 | 2.22 | ABN33422 |
| 26 | 29 | 43.8 | 5.1 | 1.517 | 2.214 | 2.22 | AAE00766 |
| 25 | 30 | 43.8 | 5.1 | 1.517 | 2.214 | 2.22 | AAE33000 |
| 24 | 31 | 43.8 | 5.1 | 1.998 | 2.214 | 2.22 | AAE33000 |
| 23 | 32 | 43.8 | 5.1 | 1.998 | 2.214 | 2.22 | AAE33000 |
| 22 | 33 | 43.4 | 5.0 | 3.474 | 2.214 | 2.22 | AAE33000 |
| 21 | 34 | 43.4 | 5.0 | 3.474 | 2.214 | 2.22 | AAE33000 |
| 20 | 35 | 43.4 | 5.0 | 3.474 | 2.214 | 2.22 | AAE33000 |
| 19 | 36 | 43.4 | 5.0 | 3.474 | 2.214 | 2.22 | AAE33000 |
| 18 | 37 | 42.6 | 4.9 | 9.98 | 2.214 | 2.22 | AAE33000 |
| 17 | 38 | 42.6 | 4.9 | 7.55 | 2.214 | 2.22 | AAE33000 |
| 16 | 39 | 42.6 | 4.9 | 9.91 | 2.214 | 2.22 | AAE33000 |
| 15 | 40 | 42.6 | 4.9 | 9.91 | 2.214 | 2.22 | AAE33000 |
| 14 | 41 | 42.6 | 4.9 | 9.91 | 2.214 | 2.22 | AAE33000 |
| 13 | 42 | 42.6 | 4.9 | 1.463 | 2.214 | 2.22 | ABA80969 |
| 12 | 43 | 42.6 | 4.9 | 1.605 | 2.214 | 2.22 | ABA80969 |
| 11 | 44 | 42.6 | 4.9 | 1.682 | 2.214 | 2.22 | AAE68922 |
| 10 | 45 | 42.6 | 4.9 | 1.683 | 2.214 | 2.22 | AAE68922 |

ALIGNMENTS

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RESULT 1
AAA64556
ID      AAA64556 standard; DNA; 864

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AAA64556;

02-JAN-2001 (first entry)

DNA sequence encoding a human B7RP1 polypeptide

CRP1; CD28 related protein-1; B7RP1; B7 related protein-1; T-lymphocyte activation; tumor necrosis factor

T-cell proliferation; T-cell mediated disorder; SS.

Abstract

CDS

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/ product= "B7RPI"

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mat_peptide

[illegible]

10-2115-2000

27-TAN-2000: 2000ISO-11501971

PR 03-FEB-1999; 9905-0244448.
 PR 08-MAR-1999; 9905-0264527.
 XX
 PA (AMGE-) AMGEN INC.
 PI Yoshinaga SK;
 XX WPI; 2000-543476/49.
 DR P-PSDB; AAB08727.
 XX
 PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 PS Claim 2; Fig 3A; 174pp; English.
 CC
 CC The present sequence encodes a B7RP1 (B7 related protein-1)
 CC polypeptide. The specification also describes a CRP1 (CD28 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 CC
 XX Sequence 864 BP; 197 A; 245 C; 250 G; 172 T; 0 other;
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 Query Match 100.0%; Score 864; DB 21; Length 864;
 Best Local Similarity 100.0%; Pred. No. 2.1e-221;
 Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | | 661 | CTTCTGCAGCAGAACCTGACTGTGCGCAGCCAGACAGAAATGACATGGAGAGAGAC | 720 |
| Db | | 661 | CTTCTGCAGCAGAACCTGACTGTGCGCAGCCAGACAGAAATGACATGGAGAGAGAC | 720 |
| Qy | | 721 | AAGATCAGAGAAATCCAGTGTACCGCGGAGAAACCGCGCCACGTGGAGCATCTCTG | 780 |
| Db | | 721 | AAGATCAGAGAAATCCAGTGTACCGCGGAGAAACCGCGCCACGTGGAGCATCTCTG | 780 |
| Qy | | 781 | GCTGTCTGTGCTGCTGCTGTGCTGTGCGGAGCCATAGAGGTGGTGTGACAGGACCA | 840 |
| Db | | 781 | GCTGTCTGTGCTGCTGCTGTGCTGTGCGGAGCCATAGAGGTGGTGTGACAGGACCA | 840 |
| Qy | | 841 | TGCTTCCACACACAGCTATGACAGT 864 | |
| Db | | 841 | TGCTTCCACACACAGCTATGACAGT 864 | |
| RESULT 2 | | | | |
| ID | ABK87593 | standard; cDNA; 864 BP. | | |
| XX | ABK87593; | | | |
| DT | 07-OCT-2002 | (first entry) | | |
| XX | CDNA encoding human B7 related protein-1 (B7RP1) #1. | | | |
| XX | CD28 related protein-1; CRP1; T-lymphocyte costimulatory protein; | | | |
| KW | B7 related protein-1; B7RP1; T-cell mediated disorder; hypersensitivity; | | | |
| KW | IGE-mediated disorder; allergy; sinus inflammation; immune disease; | | | |
| KW | graft survival; immune activation; asthma; cancer gene immunotherapy; | | | |
| KW | T-cell dependent B-cell mediated disease; leukemia; sarcoma; melanoma; | | | |
| KW | adenocarcinoma; prostate tumour; lung carcinoma; colon carcinoma; tumour; | | | |
| KW | viral infection; Hepatitis A virus; autoimmune disorder; psoriasis; | | | |
| KW | rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; | | | |
| KW | diabetes; immunethrombocytopenic purpura; toxic shock syndrome; | | | |
| KW | bone marrow; organ transplantation; inflammatory bowel disease; | | | |
| KW | allsensitisation; blood transfusion; graft vs. host disease; human; | | | |
| OS | Homo sapiens. | | | |
| XX | Key | Location/Qualifiers | | |
| XX | 1..864 | /*tag= a | | |
| XX | CD5 | /product= "B7RP1" | | |
| XX | | /note= "B7 related protein-1" | | |
| XX | | /partial | | |
| XX | | /note= "No stop codon given" | | |
| XX | WO200244364-A2. | | | |
| XX | 06-JUN-2002. | | | |
| XX | 28-NOV-2001; 2001WO-US44859. | | | |
| XX | 28-NOV-2000; 2000US-0728420. | | | |
| XX | (AMGE-) AMGEN INC. | | | |
| XX | (AMGE-) AMGEN CANADA INC. | | | |
| XX | Yoshinaga SK, Mak TW, Shahinian A, Bladt AT, Senaldi G; | | | |
| XX | WPI; 2000-547698/58. | | | |
| XX | P-PSDB; AAU99785. | | | |
| XX | Novel isolated T-lymphocyte costimulatory polypeptide, such as CD28 | | | |
| XX | related protein-1 or B7 related protein-1, useful for treating, | | | |
| XX | preventing or ameliorating a T-cell mediated disorder in an animal | | | |


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Db 84 CAGGAGGAAGAGTACAGCCATGGTAGGACGACGAGGAGCTCAGCTGCGCTTGCCCT 143
Qy 121 GAAGAACCCCTTTTGAATTAATGATGTTACGTATATTTGGCAACAGTACTCGAAA 180
Db 144 GAAGGAACCCCTTTTGAATTAATGATGTTACGTATATTTGGCAACAGTACTCGAAA 203
Qy 181 ACCGGGTGACTACACATCCACAGACAGCTCTTTGGAAAACTGGACAGCCGCTAC 240
Db 204 ACCGGGTGACTACACATCCACAGACAGCTCTTTGGAAAACTGGACAGCCGCTAC 263
Qy 241 CGGAACCGAGCCCTGATGATCACCAGCCGATGCTGGCGGGGAGCTTCTCCCTGCGCTG 300
Db 264 CGGAACCGAGCCCTGATGATCACCAGCCGATGCTGGCGGGGAGCTTCTCCCTGCGCTG 323
Qy 301 TTCAACGTACACCCCGAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 360
Db 324 TTCAACGTACACCCCGAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 383
Qy 361 GGATTCCAGAGGTTTGAAGGTTGAGGTTTACACTGATGCTGAGCAGAAACTTACGCTG 420
Db 384 GGATTCCAGAGGTTTGAAGGTTGAGGTTTACACTGATGCTGAGCAGAAACTTACGCTG 443
Qy 421 CCCGTGTCAGAGCCGCCCCAGAGCCCTCCAGAGATGAGTCACTTACAGTATACATCC 480
Db 444 CCCGTGTCAGAGCCGCCCCAGAGCCCTCCAGAGATGAGTCACTTACAGTATACATCC 503
Qy 481 ATTAAGGCTACCCCGAGAGAGAGAGTACTGATCAATAAGAGAGAGAGAGAGAGAGAG 540
Db 504 ATTAAGGCTACCCCGAGAGAGAGAGTACTGATCAATAAGAGAGAGAGAGAGAGAGAG 563
Qy 541 GACGAGGCTGTCAGAAATGACACAGCTTCTTGAACAATGGGGGCTTGTATAGCTGTC 600
Db 564 GACGAGGCTGTCAGAAATGACACAGCTTCTTGAACAATGGGGGCTTGTATAGCTGTC 623
Qy 601 AGCGTGTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 624 AGCGTGTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 683
Qy 661 CTTCGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 684 CTTCGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
Qy 721 AAGATCAGAGAGATCAGTACAGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 744 AAGATCAGAGAGATCAGTACAGTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803
Qy 781 GCTGTCTGTGCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 804 GCTGTCTGTGCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 863
Qy 841 TGCCTCCACACAGCTATGCAAGT 864
Db 864 TGCCTCCACACAGCTATGCAAGT 887

RESULT 5
AAA64557
ID AAA64557 standard; DNA: 1294 Bp.
XX
AC AAA64557;
XX
DT 02-JAN-2001 (first entry)
XX
DE DNA sequence encoding a human B7RP1 polypeptide.
XX
KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
T-lymphocyte activation; type I transmembrane protein; T cell activation;
T cell proliferation; T-cell mediated disorder; ss.
OS Homo sapiens.
XX
FH key Location/Qualifiers
```

```
FT 5'UTR 1..199
FT CDS /*tag- a
FT 200..1108
FT /*tag- b
FT /*product- "B7RP1"
FT sig-peptide 200..247
FT /*tag- c
FT /*tag- d
FT mat-peptide 248..1105
FT /*tag- d
PN MO200046240-A2.
XX
XX 10-AUG-2000.
XX
XX 27-JAN-2000; 2000WO-US01871.
XX
XX 03-FEB-1999; 99US-0244448.
XX
XX 08-MAR-1999; 99US-0264527.
XX
XX (AMGE-) AMGEN INC.
XX
XX yoshihaga SK;
XX
XX MPI: 2000-543476/49.
XX
XX P-PSDB; AAB08729.
XX
XX Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
XX in the treatment, prevention and diagnosis of T cell mediated disorders
XX
XX Claim 2; Fig 12A; 174pp; English.
XX
XX The present sequence encodes a B7RP1 (B7 related protein-1)
XX polypeptide. The specification also describes a CRP1 (CD28 related
XX protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
XX activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
XX predicted to be a type I transmembrane protein. The nucleic acids are
XX useful for regulating T cell activation or proliferation in an animal.
XX The polypeptides are useful for treating, preventing ameliorating or
XX diagnosing a T-cell mediated disorder in an animal. They can also be
XX used to identify test molecules that bind to the polypeptides.
XX
XX Sequence 1294 Bp; 262 A; 400 C; 392 G; 240 T; 0 other:
XX
XX Query Match 100.0%; Score 864; DB 21; Length 1294;
XX Best Local Similarity 100.0%; Pred. No. 2,4e-221;
XX Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGCGGCTGGGAGAGTCTGAGTCTGCTCTGCTCTTCTTACAGAGCTTGAAGTACT 60
XX 200 ATGCGGCTGGGAGAGTCTGAGTCTGCTCTGCTCTTCTTACAGAGCTTGAAGTACT 259
XX
XX 61 CAGGAGAAAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
XX 260 CAGGAGAAAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319
XX
XX 121 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTTGCAAAACAGTACGAAA 180
XX 320 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTATATTTGCAAAACAGTACGAAA 379
XX
XX 181 ACCGTGTGACCTTACACATCCACAGAAACAGCTCTTGGAAAAAGTGGAGAGCCGCTAC 240
XX 380 ACCGTGTGACCTTACACATCCACAGAAACAGCTCTTGGAAAAAGTGGAGAGCCGCTAC 439
XX
XX 241 CGGAACCGAGCCCTGATGATCACCAGCCGATGCTGGCGGGGAGCTTCTCCCTGCGCTG 300
XX 440 CGGAACCGAGCCCTGATGATCACCAGCCGATGCTGGCGGGGAGCTTCTCCCTGCGCTG 499
XX
XX 301 TTCAACGTACACCCCGAGAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 360
XX 500 TTCAACGTACACCCCGAGAGAGAGAGAAAGTTTCACTGCTGATGTTGAGCCAAATCCCTG 559
XX
XX 361 GGATTCCAGAGGTTTGAAGGTTTGAAGTATACACTGATGCTGAGCAGAAACTTACGCTG 420
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DB 560 GATATCCAGAGAGTTTGTAGCGTTGACATGATGTGGACGAACCTTCAGCGG 619
OY 421 CCCGTCGTAGCGCCGCCACAGCCCCCTCCAGATGAGCTACTCTTACCTGATACC 480
DB 620 CCCGTCGTAGCGCCGCCACAGCCCCCTCCAGATGAGCTACTCTTACCTGATACC 679
OY 481 ATAAAGGGGTACCCAGGCGCCCAAGCTGTACTGATCAATTAAGAGGACAGCCTGCTG 540
DB 680 ATAAAGGGGTACCCAGGCGCCCAAGCTGTACTGATCAATTAAGAGGACAGCCTGCTG 739
OY 541 GACCAAGGCTCTGCAAGATGACACCGCTCTTGAACATGCGGGGCTTGTATGACGTGTC 600
DB 740 GACCAAGGCTCTGCAAGATGACACCGCTCTTGAACATGCGGGGCTTGTATGACGTGTC 799
OY 601 AACGTCGTAGATGCGCAGGAGCCGCCAGCTGATGACATGCGTGGCATTAAGAACTG 660
DB 800 AACGTCGTAGATGCGCAGGAGCCGCCAGCTGATGACATGCGTGGCATTAAGAACTG 859
OY 661 CTTCTGACAGCAACCTGACTGTGCGCAGCAGACAGAAATGACATCGAGAGAGAGAC 720
DB 860 CTTCTGACAGCAACCTGACTGTGCGCAGCAGACAGAAATGACATCGAGAGAGAGAC 919
OY 721 AAGATCACAGAGAAATCAGTACATGACGCGGCGAGAAAAACCGCGCCACGTGAGACATCTG 780
DB 920 AAGATCACAGAGAAATCAGTACATGACGCGGCGAGAAAAACCGCGCCACGTGAGACATCTG 979
OY 781 GCGTCCTGTGCTGCTGTGGTGGCGGGGCGGATGAGGCTGGGTGACAGAGACCGA 840
DB 980 GCGTCCTGTGCTGCTGTGGTGGCGGGGCGGATGAGGCTGGGTGACAGAGACCGA 1039
OY 841 TGCCTCCAAACAGAGCTATGACAGCT 864
DB 1040 TGCCTCCAAACAGAGCTATGACAGCT 1063

RESULT 6
ABK87594
ID ABK87594 standard; cDNA: 1294 BP.
XX
AC ABK87594;
XX
DT 07-OCT-2002 (first entry)
XX
DE cDNA encoding human B7 related protein-1 (B7RP1) #2.
XX
KM CD28 related protein-1; CRP1; T-lymphocyte costimulatory protein;
KM B7 related protein-1; B7RP1; T-cell mediated disorder; hypersensitivity;
KM IgE-mediated disorder; allergy; sinus inflammation; immune disease;
KM graft survival; immune activation; asthma; cancer gene immunotherapy;
KM adenocarcinoma; prostate tumour; lung carcinoma; colon carcinoma; tumour;
KM viral infection; Hepatitis A virus; autoimmune disorder; psoriasis;
KM rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KM diabetes; immunethrombocytopenic purpura; toxic shock syndrome;
KM bone marrow; organ transplantation; inflammatory bowel disease;
KM atherosclerosis; blood transfusion; graft vs. host disease; human;
KM gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 200..1108
FT /tag a
FT /product "B7RP1"
FT /note="B7 related protein-1"
XX
PN W0200244364-A2.
XX
PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001MO-US44859.

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PR 28-NOV-2000; 2000US-0728420.
XX
XX (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
XX
XX Yoshinaga SK, Mak TW, Shahinian A, Bladt AT, Senaldi G;
XX WPI; 2002-547698/58.
DR P-PSDB; AAU99789.
XX
XX Novel isolated T-lymphocyte costimulatory polypeptide, such as CD28
PT related protein-1 or B7 related protein-1, useful for treating,
PT preventing or ameliorating a T-cell mediated disorder in an animal
XX
XX Claim 2: Fig 12A; 197p; English.

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The invention describes an isolated T-lymphocyte costimulatory polypeptide (I), such as CD28 related protein-1 (CRP1) or B7 related protein-1 (B7RP1), and orthologues, allelic variants or alternatively sliced variants of these sequences. (I) is useful for treating, preventing, ameliorating or diagnosing a T-cell mediated disorder or a susceptibility to a T-cell mediated disorder in an animal. (I) is useful for identifying a test molecule which binds to (I) by contacting (I) with a test molecule, and determining the extent of binding of (I) to the test molecule. The method further comprises determining the activity of (I) when bound to the compound. An anti-(I) antibody is useful for suppressing an immune response in an animal, for decreasing IgE production in an animal or for treating an IgE-mediated disorder such as asthma, allergies, hypersensitivity and sinus inflammation. (I) and anti-(I) antibodies are useful for treating immune disease, graft survival, immune activation, T-cell dependent B-cell mediated disease, cancer gene immunotherapy (for e.g. leukemias, sarcomas, melanomas, adenocarcinomas, prostate tumours, lung carcinomas, colon carcinomas and other tumours), viral infection (e.g. by Hepatitis A virus), autoimmune disorders (such as rheumatoid arthritis, psoriasis, multiple sclerosis, diabetes, systemic lupus erythematosus and immunethrombocytopenic purpura), toxic shock syndrome, bone marrow and organ transplantation, inflammatory bowel disease, atherosclerosis and for regulating the interaction of B7RP1 or CRP1. This sequence encodes the human B7 related protein-1 (B7RP1) a novel protein of the T-cell costimulatory pathway.

Sequence 1294 BP; 262 A; 400 C; 392 G; 240 T; 0 other;

Query Match 100.0%; Score 864; DB 24; Length 1294;
 Best Local Similarity 100.0%; Pred. No. 2.4e-221;
 Matches 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ATGCGGCTGGGAGAGCTGAGCTGCTCTGCTCTTCTGAGAGCTTGTGAGCTGATCT 60
DB 200 ATGCGGCTGGGAGAGCTGAGCTGCTCTGCTCTTCTGAGAGCTTGTGAGCTGATCT 259
OY 61 CAGGAGAGAGAGTCTAGAGCGATGTAGCAGGAGCGTGAAGTCACTGCGCTTGCCCT 120
DB 260 CAGGAGAGAGAGTCTAGAGCGATGTAGCAGGAGCGTGAAGTCACTGCGCTTGCCCT 319
OY 121 GAAGGAGCCGTTTATTTAAATGATGTTTACGTATTTGGCAACCGTAGTCGAA 180
DB 320 GAAGGAGCCGTTTATTTAAATGATGTTTACGTATTTGGCAACCGTAGTCGAA 379
OY 181 ACCGTGAGCTACACCATCCACAGAGAGCTCTTGGAAACGTGAGACGCGCTAC 240
DB 380 ACCGTGAGCTACACCATCCACAGAGAGCTCTTGGAAACGTGAGACGCGCTAC 439
OY 241 CCGAACCAGCCCTGATGTACACGCGCGCATGCTGCGGAGCACTTCTCCCTGCGCTTG 300
DB 440 CCGAACCAGCCCTGATGTACACGCGCGCATGCTGCGGAGCACTTCTCCCTGCGCTTG 499
OY 301 TTCACGTACCCCGCAGAGCAGAGAGTTCACATGCTGCTGTTGAGCCAAATCCCTG 360
DB 500 TTCACGTACCCCGCAGAGCAGAGAGTTCACATGCTGCTGTTGAGCCAAATCCCTG 559

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| | | | |
|----------|---|---|------|
| OY | 361 | GGATTCCAGAGAGGTTTTAGCGTTGAGGTTACACTGCATGTGGCAGCAAACTTCACGCTG | 420 |
| Db | 560 | GGATTCCAGAGAGGTTTTAGCGTTGAGGTTACACTGCATGTGGCAGCAAACTTCACGCTG | 619 |
| OY | 421 | CCCGTCTGACAGGCCCCCACCAGGCCCTCCAGGATGAGCTCACTTCAGCTGTACATCC | 480 |
| Db | 620 | CCCGTCTGACAGGCCCCCACCAGGCCCTCCAGGATGAGCTCACTTCAGCTGTACATCC | 679 |
| OY | 481 | ATMAAGGCTACCCAGGCCCCACGCTGACTGATCAATTAAGACGGACAACAGCCTGCTG | 540 |
| Db | 680 | ATMAAGGCTACCCAGGCCCCACGCTGACTGATCAATTAAGACGGACAACAGCCTGCTG | 739 |
| OY | 541 | GACGAGGCTCTGCAGAAATGACACCGTCTTCTTGAACATGCGGGGGCTTGATGACGCGTC | 600 |
| Db | 740 | GACGAGGCTCTGCAGAAATGACACCGTCTTCTTGAACATGCGGGGGCTTGATGACGCGTC | 799 |
| OY | 601 | ACCGTCTGAGGAGTCGACGAGACCCCCAGCGTGAACATTGGCTCTGCATAGAGAACGTG | 660 |
| Db | 800 | ACCGTCTGAGGAGTCGACGAGACCCCCAGCGTGAACATTGGCTCTGCATAGAGAACGTG | 859 |
| C | 661 | CTTTCGACGAGAAACCTACTGTGTGGGAGCGACAGACAGAAATGACATTCGGAGAGAGAC | 720 |
| Db | 860 | CTTTCGACGAGAAACCTACTGTGTGGGAGCGACAGACAGAAATGACATTCGGAGAGAGAC | 919 |
| OY | 721 | AAGATCACAGAGAAATCCAGTCACTACGCGGAGAAAAACCGGCCACGTGGAGCATCTCG | 780 |
| Db | 920 | AAGATCACAGAGAAATCCAGTCACTACGCGGAGAAAAACCGGCCACGTGGAGCATCTCG | 979 |
| OY | 781 | GCTGTCTGTGCTCCCTGCTTGTGTGTGTGTGGCGGTGGCCATTAGCTGGGTGTGCAGGGACGA | 840 |
| Db | 980 | GCTGTCTGTGCTCCCTGCTTGTGTGTGTGTGGCGGTGGCCATTAGCTGGGTGTGCAGGGACGA | 1033 |
| OY | 841 | TGCCCTCAACACAGCTATGCAAGT 864 | |
| Db | 1040 | TGCCCTCAACACAGCTATGCAAGT 1063 | |
| RESULT 7 | | | |
| KM | AAH77870 | | |
| ID | AAH77870 | standard; cDNA: 1453 BP. | |
| AC | AAH77870; | | |
| XX | | | |
| DT | 13-NOV-2001 | (first entry) | |
| XX | | | |
| DE | Nucleotide sequence of a human hb7-H2 polypeptide. | | |
| XX | | | |
| KM | hb7-H2; T cell stimulator; immunosuppression; cancer; AIDS; | | |
| KM | congenital immune deficiency; cellular immune response; | | |
| KM | inflammatory condition; autoimmune disease; rheumatoid arthritis; | | |
| XX | multiple sclerosis; insulin-dependent diabetes mellitus; ss. | | |
| OS | Homo sapiens. | | |
| XX | | | |
| Key | Location/Qualifiers | | |
| FT | 51..959 | | |
| FT | CDS | | |
| FT | /tag- a | | |
| FT | /product- "hb7-H2" | | |
| FT | 51..113 | | |
| FT | /tag- b | | |
| XX | | | |
| PN | MO200164704-Al. | | |
| XX | | | |
| PD | 07-SEP-2001. | | |
| XX | | | |
| PE | 02-MAR-2001; 2001MO-US06769. | | |
| XX | | | |
| PR | 02-MAR-2000; 2000US-0186519. | | |
| XX | | | |
| PA | (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES. | | |
| XX | | | |
| PI | Chen L; | | |
| IX | | | |

| | |
|-----------------------|--|
| DR | WPI: 2001-514837/56. |
| XX | P-PSDB: AAG67292. |
| DR | An isolated DNA encoding a hb7-H2 polypeptide, useful for treating |
| XX | cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis, |
| PT | multiple sclerosis or insulin-dependent diabetes mellitus) - |
| XX | |
| XX | Example 2: Fig 2a: 50pp: English. |
| XX | |
| CC | The present sequence encodes a human polypeptide, designated hb7-H2. The |
| CC | hb7-H2 polypeptide co-stimulates T cells. The hb7-H2 proteins and its |
| CC | variants are generally useful as immune response-stimulating |
| CC | therapeutics. For example, the polypeptides can be used for treatment |
| CC | of disease conditions characterized by immunosuppression, e.g., cancer, |
| CC | AIDS or AIDS-related complex, either virally or environmentally-induced |
| CC | conditions, and certain congenital immune deficiencies. They may also |
| CC | be employed to increase immune function that has been impaired by the |
| CC | use of radiotherapy or immunosuppressive drugs such as certain |
| CC | chemotherapeutic agents, and therefore are particularly useful when |
| CC | given in conjunction with such drugs or radiotherapy. The hb7-H2 |
| CC | nucleic acid and polypeptide can be used to treat conditions |
| CC | involving cellular immune responses, e.g., inflammatory conditions |
| CC | (such as, for example, those induced by infectious agents including |
| CC | Mycobacterium tuberculosis or M. leprae), or other pathologic |
| CC | cell-mediated responses such as those involved in autoimmune diseases |
| CC | (e.g. rheumatoid arthritis), multiple sclerosis, or insulin-dependent |
| CC | diabetes mellitus). |
| XX | |
| XX | |
| SQ | Sequence 1453 BP; 306 A; 428 C; 441 G; 278 T; 0 other: |
| Query Match | 100.0%; Score 864; DB 22; Length 1453; |
| Best Local Similarity | 100.0%; Pred. No. 2.5e-221; |
| Matches | 864; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 ATGCGGCTGGCAGTCTGACTGCTCTTCCTGCTCTTACGACGCTTGACTGATCT 60 |
| DB | 51 ATGCGGCTGGGAGTCTGGAGCTGCTCTTCCTGCTCTTACGACGCTTGACTGATCT 110 |
| QY | 61 CAGGAGGAAGAGTACAGACGATGTGAGGACGACGAGTGCAGCTCAGCTGGCCTTCCCT 120 |
| DB | 111 CAGGAGGAAGAGTACAGACGATGTGAGGACGACGAGTGCAGCTCAGCTGGCCTTCCCT 170 |
| QY | 121 GAGGAGAGCGCTTTTGATTTAAATGATGTTTACGATATTTGGCAAAACGATGATCGAAA 180 |
| DB | 171 GAGGAGAGCGCTTTTGATTTAAATGATGTTTACGATATTTGGCAAAACGATGATCGAAA 230 |
| QY | 181 ACCGATGAGCTTACCATCTCCACAGAAACACTCTCTGGAAAAGGTGACAGCGGTAC 240 |
| DB | 231 ACCGATGAGCTTACCATCTCCACAGAAACACTCTCTGGAAAAGGTGACAGCGGTAC 290 |
| QY | 241 CGGAACCGAGCCCTGATGTACCGCGGCATGTGCGGGGGGAGCTTCCCTGCGCTTG 300 |
| DB | 291 CGGAACCGAGCCCTGATGTACCGCGGCATGTGCGGGGGGAGCTTCCCTGCGCTTG 350 |
| QY | 301 TTCAACGTCACCCCCCAGAGACGACGAGAAAGTTTCACTGCTGTGTGAGCCAATCCCTG 360 |
| DB | 351 TTCAACGTCACCCCCCAGAGACGACGAGAAAGTTTCACTGCTGTGTGAGCCAATCCCTG 410 |
| QY | 361 GGATTCACAGAGAGTTTGTAGCTGTAGAGTTACATGCAATGTGGACAAACTTCAGCGTG 420 |
| DB | 411 GGATTCACAGAGAGTTTGTAGCTGTAGAGTTACATGCAATGTGGACAAACTTCAGCGTG 470 |
| QY | 421 CCGCTGTACAGCGCCCCCACAAGCCCTTCCAGAGATGAGCTCACCTTCAGCTGTACATCC 480 |
| DB | 471 CCGCTGTACAGCGCCCCCACAAGCCCTTCCAGAGATGAGCTCACCTTCAGCTGTACATCC 530 |
| QY | 481 ATTAACGGCTACCCAGAGCCCAAGGTGTACGTGATCAATTAAGAGGACAAACGCTGCTG 540 |
| DB | 531 ATTAACGGCTACCCAGAGCCCAAGGTGTACGTGATCAATTAAGAGGACAAACGCTGCTG 590 |
| QY | 541 GACCAAGCTGTGCAAAATGACACCTCTTCTTGAAATCAGCGGCGCTTATGACGTGTGTC 600 |
| DB | 591 GACCAAGCTGTGCAAAATGACACCTCTTCTTGAAATCAGCGGCGCTTATGACGTGTGTC 650 |

| | | | |
|----|-----|---|-----|
| Qy | 601 | AGTTCGTGAGAGATCGACGAGACCCCCAGCGTGAACATTGGCTGCTGCATAGAGAACGTC | 660 |
| | | | |
| Db | 651 | AGCGTCTGAGAGATCGACGAGACCCCCAGCGTGAACATTGGCTGCTGCATAGAGAACGTC | 710 |
| Qy | 661 | CTTCTGCAGCAGAACTGACTGTCTGGCAGCCAGACAGAGAAATACATCGGAGAGAGAGAC | 720 |
| Db | 711 | CTTCTGCAGCAGAACTGACTGTCTGGCAGCCAGACAGAGAAATACATCGGAGAGAGAGAC | 770 |
| Qy | 721 | AAGATCACAGAGATCCAGTCAGTACCGCGGAGAAAAACCGCGGCACGTGGACATCTCTG | 780 |
| Db | 771 | AAGATCACAGAGATCCAGTCAGTACCGCGGAGAAAAACCGCGGCACGTGGACATCTCTG | 830 |
| Qy | 781 | GCTTCCCTGTGCTCGCTTGTGTGTGTGGCCGTGGCCATAGGCTGGGATGTACAGGACCGCA | 840 |
| Db | 831 | GCTTCCCTGTGCTCGCTTGTGTGTGTGGCCGTGGCCATAGGCTGGGATGTACAGGACCGCA | 890 |
| Qy | 841 | TGCTCCACACAGCTATGCAAGGT | 864 |
| | | | |
| | | | |
| | | TGCTCCACACAGCTATGCAAGGT | 914 |

| | |
|-------------|--------------------------|
| RESULT 8 | |
| AAS00423 | |
| ID AAS00423 | standard; cDNA; 1548 BP. |

DT 11-MAY-2001 (first entry)

Human B7-3 cDNA.

KM Human: I-35. Inducible co-stimulatory; ICOS; η -D; KIAA0653; CD28.
KM T-cell; ICOS-mediated activity; IL-10 production; T12 activity;
KM Helicobacter pylori induced peptic ulcer; Cronin's disease.
KM multiple sclerosis; type 1 diabetes mellitus; graft rejection.
KM helminth infection; allergic diseases; ss.

OS Homo sapiens.

| | | |
|----|-----|---------------------|
| FH | Key | Location/Qualifiers |
| FT | CDS | 1..1548 |

FT /note= "This sequence does not contain a stop codon"

PN WO200112658-A2.

22-FEB-2001.

10-AUG-2000; 2000WO-GB03079.

PR 11-AUG-1999; 99US-0148402.

PA (ISIS-) ISIS INNOVATIONS LTD.

PI Davis S.

WPT: 2001-226547/23.

DN F F3DB, MA000422.
XX

PT New B/-3 polypeptides useful for modulating inducible co-stimulator protein and for treating Crohn's disease multiple sclerosis

P1 diabetes mellitus, infections and allergic diseases

Claim 35; page 67; 77pp; English.

CC The present sequence encodes for a novel human B7-3 protein which a

CC previously referred to as TU-D or KIAA0653 was considered by the 2

CC sequence to be complete and renamed the sequence as B7-3. Also described

CC is a soluble form of B7-3 (AAU00423) which comprises the B7-3 signal
CC sequence and extracellular domain. The extracellular domain is shown to
CC bind ICOS which is related to CD28 and expressed on T-cells. B7-3
CC polypeptides or its fragments are useful for identifying a substance
CC which interacts with the polypeptide or its fragment. B7-3 polypeptides,
CC fragments, tetramer, an agent with an ability to affect B7-3 activity or
CC a specific binding member are useful for modulating an ICOS-mediated
CC activity of T-cells by modulating IL-10 production and TH2 activity, and
CC for manufacturing a medicament for modulating an ICOS-mediated activity
CC of T-cells. B7-3 polypeptides are useful for development of diagnostic,
CC prophylactic and therapeutic agents for diseases such as Helicobacter
CC pylori induced peptic ulcers, Crohn's disease, multiple sclerosis, type
CC II diabetes mellitus, graft rejection, helminth infections, and allergic
CC diseases.

SQ Sequence 1548 BP; 303 A; 472 C; 484 G; 289 T; 0 other;

| | | | | |
|---------------------------|---------|--------------------|-----------|--------------|
| Query Match | 100.0% | Score 864; | DB 22; | Length 1548; |
| Best Local Similarity | 100.0%; | Pred. No. 2.5e+22; | | |
| Matches 864; Conservative | 0; | Mismatches 0; | Indels 0; | Gaps 0 |

| | | | |
|----|-----|--|-----|
| QY | 1 | ATGGGGGCGGGGAGTCGCGGMACTGCTCTTCCCTGCTTTACACACACTCTTGAGGCTGAACT | 60 |
| Db | 1 | ATGGCGGCTGGGGAGTCCTGGACTGCTCTTCTCTGCTCTTACACAGCTTTCAGCTGAACT | 60 |
| QY | 61 | CAGGAGAAGGAAGTCAGAGCATGGTTAGGCGACGACGTGAGGCTGCGCTGGCTTGCCT | 120 |
| Db | 61 | CAGGAGAAGGAAGTCAGAGCATGGTTAGGCGACGACGTGAGGCTGCGCTGGCTTGCCT | 120 |
| QY | 121 | GAGGAGAAGCCGTTTTGATTTAAATGATGTTTACGTATATTTGGCAACCACTGAGTGCAAA | 180 |
| Db | 121 | GAGGAGAAGCCGTTTTGATTTAAATGATGTTTACGTATATTTGGCAACCACTGAGTGCAAA | 180 |
| QY | 181 | ACCGGGGAGACTACCAACATCCACAGAACGTCCTTTGGAAAACGTGGACGCGCTAC | 240 |
| Db | 181 | ACCGGGGAGACTACCAACATCCACAGAACGTCCTTTGGAAAACGTGGACGCGCTAC | 240 |
| QY | 241 | CGGAACCCAGCCCTGATGTACACGGGCGGCATGCTGGGCGGGCGACTTCTCCCTGGCTTG | 300 |
| Db | 241 | CGGAACCCAGCCCTGATGTACACGGGCGGCATGCTGGGCGGGCGACTTCTCCCTGGCTTG | 300 |
| QY | 301 | TTTCAACGTACCCCCCAGAGCAGACAGAAATTTACATGCTCCTGTTGAGCCAAATCCCTG | 360 |
| Db | 301 | TTTCAACGTACCCCCCAGAGCAGACAGAAATTTACATGCTCCTGTTGAGCCAAATCCCTG | 360 |
| QY | 361 | GGATTTCAGAGAGTTTGTAGCGTTAGGTTACATGCATGTGGGAGCAAACTTCAGCGTG | 420 |
| Db | 361 | GGATTTCAGAGAGTTTGTAGCGTTAGGTTACATGCATGTGGGAGCAAACTTCAGCGTG | 420 |
| QY | 421 | CCCGTCGACAGGGCCCCCAGAGCCCTCCAGAGATGAGCTCACCTTTCACGTGATATCC | 480 |
| Db | 421 | CCCGTCGACAGGGCCCCCAGAGCCCTCCAGAGATGAGCTCACCTTTCACGTGATATCC | 480 |
| QY | 481 | ATTAACGGGCTACCCAGGCGCCAAAGTGTACTTGATCAATAAGACGCAACAGGCTGCTG | 540 |
| Db | 481 | ATTAACGGGCTACCCAGGCGCCAAAGTGTACTTGATCAATAAGACGCAACAGGCTGCTG | 540 |
| QY | 541 | GACCAAGGCTCTGCAGAATGACACCGTCTTCTTGAACAATGGGGGCTGTGTAAGGTGTC | 600 |
| Db | 541 | GACCAAGGCTCTGCAGAATGACACCGTCTTCTTGAACAATGGGGGCTGTGTAAGGTGTC | 600 |
| QY | 601 | ACCGTGTGAGAGATGGACGCGACCCCGACGCTGGAACATTTGGCTCTGCTATAGAAACGTG | 660 |
| Db | 601 | ACCGTGTGAGAGATGGACGCGACCCCGACGCTGGAACATTTGGCTCTGCTATAGAAACGTG | 660 |
| QY | 661 | CTTCTGCAGCAGAACTTACTGTGTGGCAGCCAGACAGAGAAATGACATCGGAGAGAGAC | 720 |
| Db | 661 | CTTCTGCAGCAGAACTTACTGTGTGGCAGCCAGACAGAGAAATGACATCGGAGAGAGAC | 720 |
| QY | 721 | AAGATCACAGAGATCCAGTACAGTACGGGCGAGAAAAACGGCCACAGTGGAGCATCTTG | 780 |
| Db | 721 | AAGATCACAGAGATCCAGTACAGTACGGGCGAGAAAAACGGCCACAGTGGAGCATCTTG | 780 |

Oy 7b1 .GCTGTCCTGCTGCTGCTGCTGCGGTCATAGCTGCGTGTGACAGGACCGA 840
Db 7b1 GCTGTCCTGCTGCTGCTGCTGCTGCGGTCATAGCTGCGTGTGACAGGACCGA 840
Oy 841 TGCTCTCAACACAGCTATGACAGT 864
Db 841 TGCTCTCAACACAGCTATGACAGT 864

RESULT 9
ABAO6726
ID ABAO6726 standard; cDNA: 2114 BP.
XX
XX ABAO6726;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human cDNA SEQ ID NO: 392.
XX
XX Human; gene therapy; neural disorder; immune system disorder;
K muscular disorder; reproductive disorder; gastrointestinal disorder;
K pulmonary disorder; cardiovascular disorder; renal disorder;
KM proliferative disorder; inflammation; ss.
XX
OS Homo sapiens.
XX
PN MO200154474-A2.
PD
XX 02-AUG-2001.
XX
PE 17-JAN-2001; 2001MO-US01349.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 24-FEB-2000; 2000US-184664P.
PR 02-MAR-2000; 2000US-186350P.
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PR 17-MAR-2000; 2000US-190076P.
PR 18-APR-2000; 2000US-198123P.
PR 19-MAY-2000; 2000US-205515P.
PR 07-JUN-2000; 2000US-209467P.
PR 28-JUN-2000; 2000US-214886P.
PR 30-JUN-2000; 2000US-215135P.
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PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
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PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225213P.
PR 14-AUG-2000; 2000US-225214P.
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PR 18-AUG-2000; 2000US-226279P.
PR 22-AUG-2000; 2000US-226681P.
PR 22-AUG-2000; 2000US-226888P.
PR 22-AUG-2000; 2000US-227182P.
PR 23-AUG-2000; 2000US-227009P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.

PR 05-SEP-2000; 2000US-229513P.
PR 06-SEP-2000; 2000US-230437P.
PR 06-SEP-2000; 2000US-230438P.
PR 08-SEP-2000; 2000US-231242P.
PR 08-SEP-2000; 2000US-231243P.
PR 08-SEP-2000; 2000US-231244P.
PR 08-SEP-2000; 2000US-231413P.
PR 08-SEP-2000; 2000US-231414P.
PR 08-SEP-2000; 2000US-232081P.
PR 08-SEP-2000; 2000US-232081P.
PR 12-SEP-2000; 2000US-231968P.
PR 14-SEP-2000; 2000US-232387P.
PR 14-SEP-2000; 2000US-232388P.
PR 14-SEP-2000; 2000US-232399P.
PR 14-SEP-2000; 2000US-232400P.
PR 14-SEP-2000; 2000US-232401P.
PR 14-SEP-2000; 2000US-233063P.
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PR 14-SEP-2000; 2000US-233065P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.
PR 25-SEP-2000; 2000US-234998P.
PR 26-SEP-2000; 2000US-235484P.
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PR 27-SEP-2000; 2000US-235836P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 13-OCT-2000; 2000US-239935P.
PR 13-OCT-2000; 2000US-239937P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241221P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241786P.
PR 20-OCT-2000; 2000US-241787P.
PR 20-OCT-2000; 2000US-241808P.
PR 20-OCT-2000; 2000US-241809P.
PR 20-OCT-2000; 2000US-241826P.
PR 01-NOV-2000; 2000US-244617P.
PR 08-NOV-2000; 2000US-246475P.
PR 08-NOV-2000; 2000US-246476P.
PR 08-NOV-2000; 2000US-246477P.
PR 08-NOV-2000; 2000US-246478P.
PR 08-NOV-2000; 2000US-246523P.
PR 08-NOV-2000; 2000US-246524P.
PR 08-NOV-2000; 2000US-246525P.
PR 08-NOV-2000; 2000US-246526P.
PR 08-NOV-2000; 2000US-246527P.
PR 08-NOV-2000; 2000US-246528P.
PR 08-NOV-2000; 2000US-246532P.
PR 08-NOV-2000; 2000US-246609P.
PR 08-NOV-2000; 2000US-246610P.
PR 08-NOV-2000; 2000US-246611P.
PR 08-NOV-2000; 2000US-246613P.
PR 17-NOV-2000; 2000US-249207P.
PR 17-NOV-2000; 2000US-249208P.
PR 17-NOV-2000; 2000US-249209P.
PR 17-NOV-2000; 2000US-249210P.
PR 17-NOV-2000; 2000US-249211P.
PR 17-NOV-2000; 2000US-249212P.
PR 17-NOV-2000; 2000US-249213P.
PR 17-NOV-2000; 2000US-249214P.
PR 17-NOV-2000; 2000US-249215P.
PR 17-NOV-2000; 2000US-249216P.

CC polypeptides of the invention and can be used to treat, prevent or
CC diagnose various types of disorders such as neurological disorders,
CC cardiovascular disorders, gastrointestinal disorders, reproductive
CC disorders, immune system disorders, renal disorders, muscular disorders,
CC pulmonary disorders, proliferative disorders and cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 2114 BP; 436 A; 655 C; 625 G; 385 T; 13 other;

Query Match 100.0%; Score 863.6; DB 22; Length 2114;

Best Local Similarity 99.9%; Pred. No. 3.6e-221;
Matches 863; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCGGCTGGGAGTCCGTGAGCTGCTCTCTCTCTTCAGCAGCCTTCAGAGTACT 60
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 129 ATGCGGCTGGGAGTCCGTGAGCTGCTCTCTCTTCAGCAGCCTTCAGAGTACT 188
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 CAGGAGAGGAGTCCAGAGGAGTGTAGGAGGAGCTGAGCTGAGCTGGTGGCCT 120
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 189 CAGGAGAGGAGTCCAGAGGAGTGTAGGAGGAGCTGAGCTGAGCTGGTGGCCT 248
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 GAAGGAGCCGTTTGAATTAATGATTTAGATATTTGGCAAAACAGTGAAGTGA 180
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 249 GAAGGAGCCGTTTGAATTAATGATTTAGATATTTGGCAAAACAGTGAAGTGA 308
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 ACCGTGTGACCTTACCATCCACAGAGCTCTTCGAGAGAGAGAGAGAGAGCT 240
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 309 ACCGTGTGACCTTACCATCCACAGAGCTCTTCGAGAGAGAGAGAGAGAGCT 368
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 CGGAGAGCCGTTGATGTACCGGCGGAGTGTGGGGGAGCTCTTCGAGAGAG 300
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 369 CGGAGAGCCGTTGATGTACCGGCGGAGTGTGGGGGAGCTCTTCGAGAGAG 428
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 TTCAGCTCACCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 429 TTCAGCTCACCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 GGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 489 GGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 549 CCCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 ATTAAGGAGTACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 609 ATTAAGGAGTACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 GAGCAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 669 GAGCAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 601 AGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 729 AGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 788
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 661 CTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 789 CTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 721 AAGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 849 AAGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 781 GCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 909 GCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 841 TGCCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 864
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 969 TGCCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992

RESULT 11
ID AAF91911
XX AAF91911 standard; cDNA; 2751 BP.
XX AAF91911;
XX 22-MAY-2001 (first entry)
XX
DE Human secreted protein-encoding gene 2 cDNA clone HMWB84, SEQ ID NO:64.
XX
XX
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; schizophrenia; asthma;
KW Parkinson's disease; cognitive disorder; sepsis; diabetes; atherosclerosis;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder; infection; wound healing; vulnerability;
KW cell culture; chemotaxis; food additive;
KW binding partner identification; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN MO200118022-A1.
XX PD 15-MAR-2001.
XX PF 31-AUG-2000; 2000MO-US24008.
XX PR 03-SEP-1999; 99US-0152315.
XX PR 03-SEP-1999; 99US-0152317.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX NI J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;
XX Soppe DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DW;
XX Moore PA, Shi Y, Wei Y, Florence KA;
XX
XX WPI, 2001-203081/20.
XX P-PSDB; AAB87395.
XX
XX Nucleic acid molecules encoding human secreted proteins, used in
XX preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
XX Parkinson's diseases and cancers -
XX
XX Claim 1; Page 518; 607pp; English.
XX
XX AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted
XX protein genes, and AAB87342-AAB87413 represent the proteins they encode.
XX AAB87414-AAB87454 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 52 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angiogenic disorders, kidney disorders,
XX gastrointestinal disorders, pregnancy-related disorders, endocrine
XX disorders, and infections. The proteins can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin aging due to
XX sunburn, to maintain organs before transplantation, for supporting cell
XX culture of primary tissues, to regenerate tissues, to identify their

PR 08-NOV-2000; 2000US-246524P.
PR 08-NOV-2000; 2000US-246525P.
PR 08-NOV-2000; 2000US-246526P.
PR 08-NOV-2000; 2000US-246527P.
PR 08-NOV-2000; 2000US-246528P.
PR 08-NOV-2000; 2000US-246532P.
PR 08-NOV-2000; 2000US-246609P.
PR 08-NOV-2000; 2000US-246610P.
PR 08-NOV-2000; 2000US-246611P.
PR 08-NOV-2000; 2000US-246613P.
PR 17-NOV-2000; 2000US-249207P.
PR 17-NOV-2000; 2000US-249208P.
PR 17-NOV-2000; 2000US-249209P.
PR 17-NOV-2000; 2000US-249210P.
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PR 17-NOV-2000; 2000US-249244P.
PR 17-NOV-2000; 2000US-249245P.
PR 17-NOV-2000; 2000US-249246P.
PR 17-NOV-2000; 2000US-249255P.
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PR 17-NOV-2000; 2000US-249259P.
PR 17-NOV-2000; 2000US-249299P.
PR 17-NOV-2000; 2000US-249300P.
PR 01-DEC-2000; 2000US-250160P.
PR 01-DEC-2000; 2000US-250391P.
PR 05-DEC-2000; 2000US-251030P.
PR 05-DEC-2000; 2000US-251988P.
PR 05-DEC-2000; 2000US-256719P.
PR 06-DEC-2000; 2000US-251479P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
PR 08-DEC-2000; 2000US-251989P.
PR 08-DEC-2000; 2000US-251990P.
PR 11-DEC-2000; 2000US-254097P.
PR 05-JAN-2001; 2001US-259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Rosen CA, Barash SC, Ruben SM;
XX DR WPI, 2001-476161/51.
P-PSDB; ABB10502.
PT Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition -
XX
XX Claim 1: SEQ ID NO: 390; 859bp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
XX DNAs. These can be used in the treatment of neural, immune system,
XX muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
XX renal and proliferative disorders and inflammation. The present sequence
XX is a cDNA of the invention.
XX
XX Sequence 2622 BP; 567 A; 797 C; 768 G; 490 T; 0 other;
SO
Query Match 99.8%; Score 862.4; DB 22; Length 2622;
Best Local Similarity 99.9%; Pred. No. 8..2e-221;
Matches 863; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ATGCGGCTGGGCAATCTGAGTCTCTCTGCTTTCAGCAGCCTTCAGCTGATACT 60
Db 130 ATGCGGCTGGGCAATCTGAGTCTCTCTGCTTTCAGCAGCCTTCAGCTGATACT 189
OY 61 CAGGAGAAGAGTCAAGCAGATGTAGGACGACGCTGAGCTCAGCTGCGCTTGCCCT 120

Db 190 CAGGAGAAGAGTCAAGCAGATGTAGGACGACGCTGAGCTCAGCTGCGCTTGCCCT 249
OY 121 GAAGGAAGCCGTTTGGATTAAATGATGTTTACATATTTGGCAACCACTGATCCAAA 180
Db 250 GAAAGGAGCCGTTTGGATTAAATGATGTTTACATATTTGGCAACCACTGATCCAAA 309
OY 181 ACCGTGGTGAACCTTACACATCCACAGAACAGCTCCTTGGAAAAGTGGAGACGCGCTAC 240
Db 310 ACCGTGGTGAACCTTACACATCCACAGAACAGCTCCTTGGAAAAGTGGAGACGCGCTAC 369
OY 241 CGGAACCGAGCCCTGATGTACACCGGCGGCGGAGATGCGGGGCGACTTCTCCGCGCTTG 300
Db 370 CGGAACCGAGCCCTGATGTACACCGGCGGCGGAGATGCGGGGCGACTTCTCCGCGCTTG 429
OY 301 TTCAAGCTCACCCCGCAGAGACGACGACAAAGTTTACTGCTGCTGGTTGAGCCAAATCCCTG 360
Db 430 TTCAAGCTCACCCCGCAGAGACGACGACAAAGTTTACTGCTGCTGGTTGAGCCAAATCCCTG 489
OY 361 GGATTCAGAGAGTTTGGAGCGTTGAGCTTACACTGCATGAGGACGACAACTTCAGCGTG 420
Db 490 GGATTCAGAGAGTTTGGAGCGTTGAGCTTACACTGCATGAGGACGACAACTTCAGCGTG 549
OY 421 CCCGTCGTACGCGCCCGCCACAGCCCTCCAGAGATGAGCTCACCTTCAGCTGATACC 480
Db 550 CCCGTCGTACGCGCCCGCCACAGCCCTCCAGAGATGAGCTCACCTTCAGCTGATACC 609
OY 481 ATAAAGGCTTACCCAGAGCCCAACGCTACTGATTCATTAAGACGACCAACAGCTCTCTG 540
Db 610 ATAAAGGCTTACCCAGAGCCCAACGCTACTGATTCATTAAGACGACCAACAGCTCTCTG 669
OY 541 GACCAGGCTCTGCAGATGACACCGCTCTTCTTGAACATGCGGGGCTGTATGACGTGTC 600
Db 670 GACCAGGCTCTGCAGATGACACCGCTCTTCTTGAACATGCGGGGCTGTATGACGTGTC 729
OY 601 AGCGTGTGAGGATGCGACGAGACCCCGAGCGTGAACATTTGCTGCTCATAGAACGTG 660
Db 730 AGCGTGTGAGGATGCGACGAGACCCCGAGCGTGAACATTTGCTGCTCATAGAACGTG 789
OY 661 CTTCTGACGAGAACCTGCAGCTGTGCGACGACGACGAGAAATGACATTCGGAGAGAGAC 720
Db 790 CTTCTGACGAGAACCTGCAGCTGTGCGACGACGACGAGAAATGACATTCGGAGAGAGAC 849
OY 721 AAGATCAGAGAGATCCAGTCAGTACCAGGAGAGAAAACCGGCGACGTGAGCATCTG 780
Db 850 AAGATCAGAGAGATCCAGTCAGTACCAGGAGAGAAAACCGGCGACGTGAGCATCTG 909
OY 781 GCTGTCTGTGCTGCTGTTGTGTGTCGTGCGGTGCGCATTAAGCTGTGTCAGAGGACCGA 840
Db 910 GCTGTCTGTGCTGCTGTTGTGTGTCGTGCGGTGCGCATTAAGCTGTGTCAGAGGACCGA 969
OY 841 TGGCTCCACACAGCTATGACAGT 864
Db 970 TGGCTCCACACAGCTATGACAGT 993
RESULT 14
AAS28853
ID AAS28853 standard; cDNA; 2622 BP.
XX AAS28853;
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immunoglobulin encoding cDNA SEQ ID No 99.
XX
XX Immunoglobulin; primer; signal transduction pathway protein; cancer; ss;
XX antisense therapy; gene therapy; neurological disorder; renal disorder;
XX cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;
XX reproductive disorder; immune system disorder; proliferative disorder;
XX muscular disorder.
XX Homo sapiens.
OS

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XX
PN      MO200155315-A2.
XX
PD      02-AUG-2001.
XX
PF      17-JAN-2001; 2001MO-US01326.
XX
PR      31-JAN-2000; 2000US-0179065.
PR      04-FEB-2000; 2000US-0180628.
PR      24-FEB-2000; 2000US-0184664.
PR      02-MAR-2000; 2000US-0186350.
PR      16-MAR-2000; 2000US-0189874.
PR      17-MAR-2000; 2000US-0190076.
PR      18-APR-2000; 2000US-0198123.
PR      19-MAY-2000; 2000US-0205515.
PR      07-JUN-2000; 2000US-0209467.
PR      28-JUN-2000; 2000US-0214886.
PR      30-JUN-2000; 2000US-0215135.
PR      07-JUL-2000; 2000US-0216647.
PR      11-JUL-2000; 2000US-0216880.
PR      11-JUL-2000; 2000US-0217487.
PR      14-JUL-2000; 2000US-0217496.
PR      26-JUL-2000; 2000US-0218290.
PR      26-JUL-2000; 2000US-0220963.
PR      26-JUL-2000; 2000US-0220964.
PR      14-AUG-2000; 2000US-0224518.
PR      14-AUG-2000; 2000US-0224519.
PR      14-AUG-2000; 2000US-0225213.
PR      14-AUG-2000; 2000US-0225214.
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PA      (HUMA-) HUMAN GENOME SCI INC.
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PI Rosen CA, Barash SC, Ruben SM:
XX MPI, 2001-457725/49.
DR P-PDB; AAU18065.
XX
PT Isolated novel immunoglobulin polypeptide for monitoring the presence
PT and progression of diseases and for diagnosis -
XX
PS Claim 1: SEQ ID No 99; 551pp; English.
XX
CC Sequences AAS28765-AAS28877 represent cDNA molecules, which encode the
CC immunoglobulin polypeptides of the invention, and primers for the
CC polynucleotides. The polynucleotides and polypeptides can be used to
CC diagnose a pathological condition or a susceptibility to a pathological
CC condition in a subject by determining the presence or absence of a
CC mutation in a DNA sequence or determining the presence or amount of
CC expression of the protein. Alternatively the identification of a binding
CC partner to a sequence allows determination of changes in protein
CC activity. The sequences can be used as research tools for receptors or
CC other signal transduction pathway proteins that interact with the
CC polypeptides of the invention and can be used to treat, prevent or
CC diagnose various types of disorders such as neurological disorders,
CC cardiovascular disorders, gastrointestinal disorders, reproductive
CC disorders, immune system disorders, renal disorders, muscular disorders,
CC pulmonary disorders, proliferative disorders and cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
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SQ Sequence 2622 BP; 567 A; 797 C; 768 G; 490 T; 0 other;
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Matches 863; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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KW antisense therapy; gene therapy; neurological disorder; renal disorder;
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KW reproductive disorder; immune system disorder; proliferative disorder;
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RESULT 15
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ID AAS28793 standard; cDNA; 2751 BP.
XX
AC AAS28793;
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DT 07-NOV-2001 (first entry)
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DE Human immunoglobulin encoding cDNA SEQ ID No 39.
XX
XX Immunoglobulin; primer: signal transduction pathway protein; cancer; ss;
KW antisense therapy; gene therapy; neurological disorder; renal disorder;
KW cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;
KW reproductive disorder; immune system disorder; proliferative disorder;
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(HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI: 2001-457725/49.
 P-PSDB; AA018005.

Isolated novel immunoglobulin polypeptide for monitoring the presence
 and progression of diseases and for diagnosis -
 Claim 1; SEQ ID NO 39; 551pp; English.

Sequences AAS28765-AAS28877 represent cDNA molecules, which encode the
 immunoglobulin polypeptides of the invention, and primers for the
 polynucleotides. The polynucleotides and polypeptides can be used to
 diagnose a pathological condition or a susceptibility to a pathological
 condition in a subject by determining the presence or absence of a
 mutation in a DNA sequence or determining the presence or amount of a
 expression of the protein. Alternatively the identification of a binding
 partner to a sequence allows determination of changes in protein
 activity. The sequences can be used as research tools for receptors or
 other signal transduction pathway proteins that interact with the
 polypeptides of the invention and can be used to treat, prevent or
 diagnose various types of disorders such as neurological disorders,
 cardiovascular disorders, gastrointestinal disorders, reproductive
 disorders, immune system disorders, renal disorders, muscular disorders,
 pulmonary disorders, proliferative disorders and cancer.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences.

Query Match 99.8%; Score 862.4; DB 22; Length 2751;
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Db 338 GAAGGAAGCCGTTTGAATTAATGATGTTTACGTAATTTGGCAACCAAGTAGTCGAAA 397
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QY 181 ACCGTGTGACCTACCACTCCACAGACAGCTCCTTGGAAAACGTGGACAGCCGCTAC 240
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QY 241 CGGAACCGAGCCCTGATGTCACCGCGGCGATGCTGGGGGCGACTTCTCCCTGCGCTG 300
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QY 301 TTCACGTACCCCCCAGAGAGACAGAAATTCTACTGCTGTGTGAGCCATCCCTG 360
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Db 518 TTCACGTACCCCCCAGAGAGACAGAAATTCTACTGCTGTGTGAGCCATCCCTG 577
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QY 361 GGATTCCAGAGAGTTTGTAGCGGTTGAGTTTACCTGCTGATGTGGAGCAAACTTACGCTG 420
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QY 421 CCGGTCTGACGCGCCCCCAGAGCCCTCCAGATGAGCTCACCTTCACGTGTACATCC 480
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QY 481 ATAAAGGCTACCCAGGCCCCAAGCTGACTGATGATCAATAGAGGAGCAACAGCCTGCTG 540
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QY 661 CTTCTGACAGCACTGACTGTGCGAGCCAGACAGGAAATGACATCGGAGAGAGAC 720
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QY 721 AAGATCACAGAAATCCAGTCAATACCGGCGAGAAAAACGCGGCCACGTGAGCATCCTG 780
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Db 938 AAGATCACAGAAATCCAGTCAATACCGGCGAGAAAAACGCGGCCACGTGAGCATCCTG 997
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QY 781 GCTGTCTGTCTGCTGT 840
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Db 998 GCTGTCTGTCTGCTGT 1057
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QY 841 TGCCTCCACACAGATATGACAGT 864
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Db 1058 TGCCTCCACACAGATATGACAGT 1081
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Search completed: November 17, 2002, 03:44:09
Job time : 167.997 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 01:49:05 ; Search time 1632.63 Seconds

(without alignments)
15401.427 Million cell updates/sec

Title: US-09-728-421d-11

Perfect score: 864

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: gb_in:**
4: gb_om:**
5: gb_ov:**
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12: gb_sy:**
13: gb_un:**
14: gb_vl:**
15: em_ba:**
16: em_fun:**
17: em_hum:**
18: em_in:**
19: em_mu:**
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21: em_or:**
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24: em_ph:**
25: em_pl:**
26: em_ro:**
27: em_sts:**
28: em_un:**
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37: em_hlg_vrt:**
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41: em_hlgo_other:**

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 864 | 100.0 | 909 | 9 | AF216749 | AF216749 Homo sapi |
| 2 | 864 | 100.0 | 953 | 9 | AX100595 | AX100595 Sequence |
| 3 | 864 | 100.0 | 1009 | 9 | AF199028 | AF199028 Homo sapi |
| 4 | 864 | 100.0 | 1048 | 6 | AX083950 | AX083950 Sequence |
| 5 | 864 | 100.0 | 1572 | 9 | AF289028 | AF289028 Homo sapi |
| 6 | 864 | 100.0 | 4358 | 9 | AB014553 | AB014553 Homo sapi |
| 7 | 716 | 82.9 | 716 | 6 | AX083952 | AX083952 Sequence |
| 8 | 460.4 | 53.3 | 2240 | 9 | AK090492 | AK090492 Homo sapi |
| 9 | 459 | 53.1 | 2706 | 9 | IROES054 | AL355680 Homo sapi |
| 10 | 355.4 | 41.1 | 36230 | 9 | AP001059 | AP001059 Homo sapi |
| 11 | 355.4 | 41.1 | 39553 | 9 | AP001058 | AP001058 Homo sapi |
| 12 | 355.4 | 41.1 | 340000 | 9 | AP001753 | AP001753 Homo sapi |
| 13 | 299.6 | 34.7 | 2718 | 6 | AF216747 | AF216747 Mus muscu |
| 14 | 299.6 | 34.7 | 2718 | 10 | AF199027 | AF199027 Mus muscu |
| 15 | 299.6 | 34.7 | 2803 | 10 | BC029227 | BC029227 Mus muscu |
| 16 | 296.4 | 34.3 | 1759 | 6 | AX100593 | AX100593 Sequence |
| 17 | 296.4 | 34.3 | 1759 | 10 | AF394451 | AF394451 Mus muscu |
| 18 | 161.4 | 18.7 | 165 | 17 | HSMC34G04 | X88131 H. sapiens D |
| 19 | 150.8 | 17.5 | 158049 | 2 | AC015891 | AC015891 Mus muscu |
| 20 | 130.6 | 15.1 | 118361 | 2 | AC109383 | AC109383 Rattus no |
| 21 | 51 | 5.9 | 3040 | 8 | AF411248 | AF411248 Chlamydom |
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| 26 | 44.8 | 5.2 | 3177 | 10 | BC019436 | BC019436 Mus muscu |
| 27 | 44.6 | 5.2 | 141746 | 2 | CNS08C8R | AL173187 Oryza sat |
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ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens B7-related protein-1 mRNA, complete cds.
ACCESSION AF216749
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 909)
Yoshinaga,S.K., Zhang,M., Pistillo,J., Horan,T., Khare,S.D.,
Miner,K., Sonnenberg,M., Boone,T., Brankow,D., Dai,T., Delaney,J.,
Han,H., Hui,A., Kohno,T., Manoukian,R., Shih,G., Whoriskey,J.S. and

TITLE Coccia, M.A.
 Characterization of a new human B7-related protein: B7RP-1 is the ligand to the co-stimulatory protein ICOS
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 909)
AUTHORS Yoshinaga, S.K., Whoriskey, J.S. and Dai, T.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1999) Molecular Biology, Amgen Inc., One Amgen Center Drive, Thousand Oaks, CA 91320, USA
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 Best local Similarity 100.0%; Pred. No. 1,7e-180;
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 LOCUS Sequence 5 from Patent WO0121796.
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 ACCESSION AX100595
 VERSION AX100595.1 GI:13619598
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
 1 (bases 1 to 953)
 Ling, V. and Dunussi-Joannopoulos, K.
 6150 molecules and uses thereof
 Patent: WO 0121796-A 5 29-MAR-2001;
JOURNAL GENETICS INSTITUTE, INC. (US)
FEATURES
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RESULT 3
AF199028
LOCUS AF199028 1009 bp mRNA linear PRI 17-FEB-2000
DEFINITION Homo sapiens B7-like protein (GL50) mRNA, complete cds.
ACCESSION AF199028
VERSION AF199028.1 GI:6983943
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1009)
Ling, V., Wu, P.W., Flinerty, H.F., Bean, K.M., Spaulding, V.,
Myashiro, J.S., Jacobs, K.A., Hunter, S.E., Zolner, R., Thomas, J.L.,
Rouser, L.A., Leonard, J.P., Hunter, S.E., Zolner, R., Thomas, J.L.,
Cutting edge: Identification of GL50, a novel B7-like protein that
functionally binds to ICOS receptor
J. Immunol. 164 (4), 1653-1657 (2000)
JOURNAL MEDLINE
PUBMED 20126021
10657606
REFERENCE 2 (bases 1 to 1009)
Ling, V.
AUTHORS
TITLE Direct Submission

JOURNAL Submitted (26-OCT-1999) Immunology, Genetics Institute, 87
CambridgePark Drive, Cambridge, MA 02140, USA
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| Dd | | 744 | AAGATCACAGAAAATCCAGTAGTAACCGGCCGAGAAAAAGCGGCCCATCGTGACATCTGTG | 803 |
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| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE Davis,S. AUTHORS Human lcos ligand and application thereof TITLE Patent: WO 0112658-A 1 22-FEB-2001; | | | | |
| JOURNAL ISIS INNOVATION LIMITED (GB) | | | | |
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| | QY | 481 | ATAAAGGCCTAACCCAGGSCCAACGCTGACTGTAGATCAATTAAGACGAGACAAGCCTGCTG | 540 |
| | Db | 481 | ATAAAGGCTACCCAGGSCCAACGCTGACTGTAGATCAATTAAGACGAGACAAGCCTGCTG | 540 |
| | QY | 541 | GACCGGCTGTCGCAAAATAGACACGCTTTCTTTGAAACATGGGGGCTTTATGAGTGGTC | 600 |
| | Db | 541 | GACCGGCTGTCGCAAAATAGACACGCTTTCTTTGAAACATGGGGGCTTTATGAGTGGTC | 600 |
| | QY | 601 | AGCGTGTGAGGATGCGACGGAACCCCGAGCTGAAACATTGGCTGCTGCATGAGAAGCTG | 660 |
| | Db | 601 | AGCGTGTGAGGATGCGACGGAACCCCGAGCTGAAACATTGGCTGCTGCATGAGAAGCTG | 660 |
| | QY | 661 | CTTCTGCAAGCAGAACCTTACTGTGGCAGGCCAGACAGAAATGACATGGAGAGAGAGAC | 720 |
| | Db | 661 | CTTCTGCAAGCAGAACCTTACTGTGGCAGGCCAGACAGAAATGACATGGAGAGAGAGAC | 720 |
| | QY | 721 | AAGATCACAGAGAAATCCAGTCAGTACCGGCGGAGAAAAACGGGCGCACGTGGACATCCTG | 780 |
| | Db | 721 | AAGATCACAGAGAAATCCAGTCAGTACCGGCGGAGAAAAACGGGCGCACGTGGACATCCTG | 780 |
| | QY | 781 | GCTGTCTGTGCTGCTTGTGTGGTGGCGGATAGGCTGGGTGTGCAAGGAGACCA | 840 |
| | Db | 781 | GCTGTCTGTGCTGCTTGTGTGGTGGCGGATAGGCTGGGTGTGCAAGGAGACCA | 840 |
| | QY | 841 | TGCCCTCAAACACGCTATGCAGGT | 864 |
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| RESULT 5 | | | | |
| LOCUS | AF289028 | 1572 bp | mRNA | linear PRI 04-DEC-2001 |
| DEFINITION | Homo sapiens transmembrane protein B7-H2 ICOS ligand mRNA, complete cds. | | | |
| ACCESSION | AF289028 | | | |
| VERSION | AF289028.1 | | | |
| KEYWORDS | GI:9858866 | | | |
| SOURCE | . | | | |
| ORGANISM | Homo sapiens. | | | |
| | Homo sapiens. | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| REFERENCE | 1 (bases 1 to 1572) | | | |
| AUTHORS | Wang,S., Zhu,G., Chapoval,A.I., Dong,H., Tamada,K., Ni,J. and Chen,L. | | | |
| TITLE | Costimulation of T cells by B7-H2, a B7-like molecule that binds ICOS | | | |
| JOURNAL | Blood 96 (8), 2808-2813 (2000) | | | |
| MEDLINE | 20477846 | | | |
| PUBMED | 11023515 | | | |
| REFERENCE | 2 (bases 1 to 1572) | | | |
| AUTHORS | Wang,S., Zhu,G., Ni,J. and Chen,L. | | | |
| JOURNAL | Direct Submission | | | |
| | Submitted (23-JUL-2000) Immunology, Mayo Clinic, 200 First Street SW, Rochester, MN 55905, USA | | | |
| FEATURES | | | | |
| source | Location/Qualifiers | | | |
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| | VTPDEOKFHCLVSLIGFEVYLVAANFSVPVASHPSDDELFTCTS | | | |
| | INGPRNVYVIKNTSLDOALONTVFILNMGLDVVSRIARTPSVNIQCIE | | | |
| | NVLQDNLTWSQSGNDIGERDKITTEPVSTGEKNATWISLVLCILVYVAALGVN | | | |
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Db 369 CGGAGCCGAGCCCTGATGTCACCGGCGGCGATGCTGGGGGGGACATCTTCCTCGGCTTG 428
QY 301 TTCAACGTCACCCCCACGAGACGAGAGAGTTTTCACCTGCTGGTGTGAGCCAAATCCCTG 360
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QY 601 AGCGTGTGAGAGTGCAGAGGAGCCGCCAGCTGAACATTTGGCTCTCATAGAGAACCTG 660
Db 729 AGCGTGTGAGAGTGCAGAGGAGCCGCCAGCTGAACATTTGGCTCTCATAGAGAACCTG 788
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Db 969 TGCCTCCAGACAGCTATGAGAGT 992

RESULT 7
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LOCUS AX083952
DEFINITION Sequence 3 from Patent WO0112658.
ACCESSION AX083952
VERSION AK083952.1 GI:13185509
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 716)
AUTHORS Davis, S.
TITLE Human ICOS ligand and application thereof
JOURNAL Patent: WO 0112658-A 3 22-FEB-2001;
ISIS INNOVATION LIMITED (GB)
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location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 164 a 206 c 201 g 145 t
ORIGIN

Query Match 82.9%; Score 716; DB 6; length 716;
Best Local Similarity 100.0%; Pred. No. 8.4e-148;
Matches 716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GAAGGAGCGGTTTGTATTAATGATGTTTACGTATATTTGGCAAACTAGTGTGAAA 180
Db 121 GAAGGAGCGGTTTGTATTAATGATGTTTACGTATATTTGGCAAACTAGTGTGAAA 180
QY 181 ACCGTGTGACTTACCAATCCACAGACAGTCTCTTGGAAAAGTGTGACAGCCGTAC 240
Db 181 ACCGTGTGACTTACCAATCCACAGACAGTCTCTTGGAAAAGTGTGACAGCCGTAC 240
QY 241 CGGAGCCGAGCCCTGATGTACCGGCGGAGTCTGGGGGGGACCTTCTCGCGCTTG 300
Db 241 CGGAGCCGAGCCCTGATGTACCGGCGGAGTCTGGGGGGGACCTTCTCGCGCTTG 300
QY 301 TTCAACGTCACCCCCACGAGACGAGAGAGTTTCACTGCTGTGTGAGCCAAATCCCTG 360
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QY 361 GGATTCAGAGAGGTTTGTGAGGTTGAGTTACACTGCATGTGGCAGCAACTTCAGCGTG 420
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QY 421 CCCGTGTCAGCGCCCCACAGAGCCCTCCAGAGTGAAGTCACTTACGTTGATATCC 480
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QY 541 GACGAGGCTCTGAGAGTGAACACCGCTCTTGAACATGGGGGCTGTATGAGAGTGTC 600
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Db 601 AGCGTGTGAGAGTGCAGAGGAGCCGCCAGGCTGAACATTTGGCTCTCATAGAGAACCTG 660
QY 661 CTTCTGAGAGAGAACTGATGTCGAGGACAGACAGAGAAATGACATCGAGAGAG 716
Db 661 CTTCTGAGAGAGAACTGATGTCGAGGACAGACAGAGAAATGACATCGAGAGAG 716

RESULT 8
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LOCUS AK090492
DEFINITION Homo sapiens cDNA FLJ33173 fls, clone ADRGL2002191, highly similar
to Homo sapiens transmembrane protein B7-H2 ICOS ligand mRNA.
ACCESSION AK090492
VERSION AK090492.1 GI:21748666
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens adrenal gland cDNA to mRNA, clone_11b.ADRGL2
clone:ADRL2002191.
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Nishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Yamamoto, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hito, Y., Saio, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2240)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takeo Isogai, FLJ Project(HRI Team); 2-6-7

| REFERENCE AUTHORS | TITLE JOURNAL MEDLINE REFERENCE AUTHORS | source |
|---|---|---|
| 1 (sites) Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Hornischer,K., Barand,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S., Hennig,S., Riesselmann,L., Dagand,E., Wehmeier,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and Yaspo,M.L. The DNA sequence of human chromosome 21 Nature 405 (6784), 311-319 (2000) | 2 (bases 1 to 340000) Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A., Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G., Hornischer,K., Barand,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S., Hennig,S., Riesselmann,L., Dagand,E., Wehmeier,S., Borzym,K., Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and Yaspo,M.L. Direct Submission Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GPF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below) On May 30, 2000 this sequence version replaced gi:7717422. The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattori@gscl.riken.go.jp * URL: http://hgp.gscl.riken.go.jp/ and * Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/ and * Keio University School of Medicine, Molecular Biology, * Tokyo 160-8582, Japan, * e.mail: nahimizu@db-med.keio.ac.jp * URL: http://www.db.med.keio.ac.jp/ and * GPF, Dept. of Genome Analysis, * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail: info.genome@gpf.de * URL: http://genome.gpf.de/ and * Max-Planck Institute for Molecular Genetics, * Innestrasse 73, D-14195 Berlin, Germany, * e.mail: info-chr21@moigen.mpg.de * URL: http://chr21.rz-berlin.mpg.de/ AL163298: Submitted (10-Apr-2000). Location/Qualifiers 1. 340000 /organism="Homo sapiens" /db_xref="taxon:9606" <1. 69557 /organism="Homo sapiens" /db_xref="taxon:9606" | source /chromosome="21" /map="21q22.3" /clone="KB218C10, 5' partial" /clone_lib="Keio BAC library" /note="Accession No. AP001054" 41536. .164174 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KB86A5" /clone_lib="Keio BAC library" /note="Accession No. AB001523" 15575. .198625 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD6B5" /clone_lib="KUD21-D Cosmid library" 192629. .229111 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD11C9" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001055" 219221. .255474 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD1C8" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001056" 255308. .259036 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD40G11" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001057" 258938. .298491 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD9G11" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001058" 287613. .323842 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD28B11" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001059" 314505. .>340000 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21" /map="21q22.3" /clone="KUD4G11, 3' partial" /clone_lib="KUD21-D Cosmid library" /note="Accession No. AP001060" complement(559. .885) /note="LIMC" /rpt_family="LINE/L1" /rpt_type="dispersed" |

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Db 291842 GCACATCTCAGGAGGAAGTACAGAGCGATGTAGACGACGATGAGCTGAGCTGCTGC 291783

QY 112 GCTTGCCCTGAAGAACCGCTTTTGAATTAATGATGTTTACGTATATTGCAACCACT 171
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Db 291782 GCTTGCCCTGAAGAACCGCTTTTGAATTAATGATGTTTACGTATATTGCAACCACT 291723

QY 172 GAGTCGAAAACCGTGTGACTACCAATCCACAGAACAGCTCTCTGGAAAAGTGGAC 231
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Db 291722 GAGTCGAAAACCGTGTGACTACCAATCCACAGAACAGCTCTCTGGAAAAGTGGAC 291663

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LOCUS Mus musculus B7-related protein 1 mRNA, partial cds.
DEFINITION AF216747
ACCESSION AF216747.1 GI:7288510
VERSION AF216747.1
KEYWORDS
SOURCE
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
1 (bases 1 to 966)
Yoshinaga,S.K., Whoriskey,J.S., Khare,S.D., Sarmiento,U., Guo,J.,
Horan,T., Shih,G., Zhang,M., Coccia,M.A., Kohno,T.,
Tajiri-Bladt,A., Campbell,P., Chang,D., Chu,L., Dai,T., Duncan,G.,
Elliot,G.S., Hui,A., McCabe,S.M., Scully,S., Shalklee,C.L., Van,G.,
Mak,T.W. and Senaldi,G.
T-cell co-stimulation through B7RP-1 and ICOS
Nature (2000) in press
2 (bases 1 to 966)
Yoshinaga,S.K. and Dai,T.
Submitted (16-DEC-1999) Molecular Biology, Amgen, Inc., One Amgen
Center Drive, Thousand Oaks, CA 91320, USA
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BASE COUNT 247 a 256 c 229 g 234 t
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QY 74 TCAGAGCATGTAGGACGAGCATGAGCTGAGCGCTGCTCGTGAAGAGAGCGCTT 133
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Qy 361 GGATTCGAGAGAGTTTGAAGCTTGAAGTTACACTGATGAGCAGCAAACTTCAAGCTG 420
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Qy 421 CCCGTCGTACAGGCGCCCGCAGAGCCCTCCAGATGAGTCACTTCACTGATACATCC 480
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Qy 541 GACCAAGCTGACAGATGACACCGCTCTTGAACATGCGGGGCTGTATGACGTGCTC 600
Db 662 GACCAAGCTGACAGATGACACCGCTCTTGAACATGCGGGGCTGTATGACGTGCTC 721
Qy 601 AGCGTGTGAGAGTGCACGAGACCCCGCAGCTGAACATTTGCTGCTGATAGAGAGCTG 660
Db 722 AGCGTGTGAGAGTGCACGAGACCCCGCAGCTGAACATTTGCTGCTGATAGAGAGCTG 781
Qy 661 CTTCGAGCAGAACTGCTGCTGCGCAGCAGCAGAAATGACATCGGAGAGAGAGAC 720
Db 782 CTTCGAGCAGAACTGCTGCTGCGCAGCAGCAGAAATGACATCGGAGAGAGAGAC 841
Qy 721 AAGATCACAGAAATTCAGTACGAGCGGAGAAACAGGCGGCTGAGAGATCTG 780
Db 842 CAGATCACAGAAATTCAGTACGAGCGGAGAAACAGGCGGCTGAGAGATCTG 901
Qy 781 GCTGTCTGCTGCC 793
Db 902 GCTGTCTGCTGCC 914

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RESULT 3
BM543561
LOCUS BM543561 978 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6492731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726681
5', mRNA sequence.
ACCESSION BM543561
VERSION BM543561.1 GI:18774056
KEYWORDS EST.
SOURCE human.
ANIM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL NIH-MGC http://mgi.ncl.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12719 row: 1 column: 18
High quality sequence stop: 708.
location/Qualifiers
1..978

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FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726681"
/clone_11b="NIH_MGC_124"

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/tissue_type="hippocampus"
/1ab_host="DH10B"
/note="Organ: Brain; Vector: pCMV-Sport6; Site:1: EcorV
(destroyed); Site:2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcorV site is destroyed upon cloning). Average
insert size 1.4 kb. Insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 203 a 301 c 290 g 183 t 1 others
ORIGIN
Query Match 84.0%; Score 725.6; DB 13; Length 978;
Best Local Similarity 95.0%; Pred. No. 1,1e-188;
Matches 771; Conservative 0; Mismatches 39; Indels 2; Gaps 2;
Qy 1 ATCGGCTGGGCGAGTCCGTGACTGCTCTTCCCTTTCAGCAGCCTTGCAGCTGATCT 60
Db 135 ATCGGCTGGGCGAGTCCGTGACTGCTCTTCCCTTTCAGCAGCCTTGCAGCTGATCT 194
Qy 61 CAGAGAGGAAGTCAAGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 195 CAGAGAGGAAGTCAAGAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
Qy 121 GAAGGAAGCGTTTGAATTAATGATGTTTACGTATATTGGCAAAACAGTAGTCGAAA 180
Db 255 GAAGGAAGCGTTTGAATTAATGATGTTTACGTATATTGGCAAAACAGTAGTCGAAA 314
Qy 181 ACCGTGTACCTTACACATCCACAGAAACAGCTCTTGGAAACAGTAGTCGAAA 240
Db 315 ACCGTGTACCTTACACATCCACAGAAACAGCTCTTGGAAACAGTAGTCGAAA 374
Qy 241 CGGAACCGAGCCCTGATGTCACCGGCGGATGCGGGGGGAGCTTCCCTGGGCTTG 300
Db 375 CGGAACCGAGCCCTGATGTCACCGGCGGATGCGGGGGGAGCTTCCCTGGGCTTG 434
Qy 301 TTCAACGTCACCCCGCAGAGCAGAGAAATTTCACTGCTGCTGTTGAGCCAAATCCCTG 360
Db 435 TTCAACGTCACCCCGCAGAGCAGAGAAATTTCACTGCTGCTGTTGAGCCAAATCCCTG 494
Qy 361 GGATTCGAGAGAGTTTGAAGCTTGAAGTTACACTGATGAGCAGCAAACTTCAAGCTG 420
Db 495 GGATTCGAGAGAGTTTGAAGCTTGAAGTTACACTGATGAGCAGCAAACTTCAAGCTG 554
Qy 421 CCCGTCGTACAGGCGCCCGCAGAGCCCTCCAGATGAGTCACTTCACTGATACATCC 480
Db 555 CCCGTCGTACAGGCGCCCGCAGAGCCCTCCAGATGAGTCACTTCACTGATACATCC 614
Qy 481 ATAAACGCTACCCCGCAGAGCCCAAGCTGATGATCAATAAGAGCAGCAACAGCTGCTG 540
Db 615 ATAAACGCTACCCCGCAGAGCCCAAGCTGATGATCAATAAGAGCAGCAACAGCTGCTG 674
Qy 541 GACCAAGCTGACAGATGACACCGCTCTTGAACATGCGGGGCTGTATGAGAGTGTGCTC 600
Db 675 GACCAAGCTGACAGATGACACCGCTCTTGAACATGCGGGGCTGTATGAGAGTGTGCTC 734
Qy 601 AGCGTGTGAGAGTGCACAGC-ACCCCGCAGCGTGAACATTTGGCTGCTGATAGAGAACT 659
Db 735 AGCGTGTGAGAGTGCACAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 794
Qy 660 GCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
Db 795 GCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 854
Qy 720 CAAGATCAGAG-AGAATTCAGTACAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 778
Db 855 CAAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 914
Qy 779 TGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 810
Db 915 TCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 946

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RESULT 4
BI488470 816 bp mRNA linear EST 28-AUG-2001
LOCUS 60302097121 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191864 5',
DEFINITION mRNA sequence.
ACCESSION BI488470 GI:15327698
VERSION BI488470.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 816)
NIH-MGC <http://mhc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M1479 row: m column: 17
High quality sequence stop: 790.
Location/Qualifiers
1. 816
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5191864"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH MGC Library."
BASE COUNT 166 a 258 c 230 g 162 t
ORIGIN
Query Match 70.3%; Score 607.4; DB 13; Length 816;
at Local Similarity 99.0%; Pred. No. 3.6e-156;
Matches 674; Conservative 0; Mismatches 1; Indels 6; Gaps 6;

434 TTCAAGTCACCCCCCAGAGAGAGAGAAAGTTTCATGCTGCTGTGTAGCCAAATCCCTG 493
435 GGATTCACAGAGAGTTTGTAGCGTTGAGGTTCACATGCGAGGAACTTACAGGTG 420
436 GGATTCACAGAGAGTTTGTAGCGTTGAGGTTCACATGCGAGGAACTTACAGGTG 553
437 CCCGTCGTCAGAGCGCCCCCAGAGCGCCCTCCAGATGAGCTCACCTTACAGTATCC 480
438 CCCGTCGTCAGAGCGCCCCCAGAGCGCCCTCCAGATGAGCTCACCTTACAGTATCC 613
439 AT-AAAGCGTACCCAGCCCAACGCTGCTGATCATATAGACGAGCAACCA-GCCTGC 538
440 ATAAACGCTACCCAGCCCAACGCTGCTGATCATATAGACGAGCAACCA-GCCTGC 673
441 TTGACACAGCTCTGAGAAATGACACCGCTCTTGAACA-TGCCGAGGCTGTATGACGTG 597
442 TTGACACAGCTCTGAGAAATGACACCGCTCTTGAACA-TGCCGAGGCTGTATGACGTG 733
443 GTACACGCTGCT-GAGATACGACGAGACCCAGCGTG-AACATTTGCTGTCATAGAGA 655
444 GTACACGCTGCTGAGATACGACGAGACCCAGCGTG-AACATTTGCTGTCATAGAGA 793
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446 ACGTTGCTTTCGACGACAGAC 814
RESULT 5
AM377686 486 bp mRNA linear EST 04-FEB-2000
LOCUS PM2-CT0238-290999-001-f03 CT0238 Homo sapiens cDNA, mRNA sequence.
DEFINITION AM377686
ACCESSION AM377686
VERSION AM377686.1 GI:6882349
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 486)
HCGP <http://www.ludwig.org.br/ORESTES>.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM2<2-PM2-CT0238-290999-001-f03<3=1999-09-29<4=1>)
Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence stop: 485.
Location/Qualifiers
1. 486
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0238"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 112 a 140 c 136 g 98 t
ORIGIN

REFERENCE 1 (bases 1 to 448)
 HGP http://www.ludwig.org.br/ORESTES.
 AUTHORS The FAPESP/LICR Human Cancer Genome Project
 TITLE Unpublished (1999)
 JOURNAL Contact: Simpson A.J.G.
 COMMENT Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM2&t2=PM2-CT0238-290999-001-f02&t3=1999-09-29&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 5
 High quality sequence stop: 221.
 Location/Qualifiers
 1. 448

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0238"
 /dev_stage="Adult"
 /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 128 a 115 c 119 g 86 t
 ORIGIN
 Query Match 43.4%; Score 375.2; DB 10; Length 448;
 Best Local Similarity 94.2%; Pred. No. 2.3e-92;
 Matches 422; Conservative 0; Mismatches 23; Indels 3; Gaps 3;

OY 314 CCCGAGCAGCAGAAATTTCACCTGCTGTGAGCCCAATCCCTGGAGTCCAGAGG 373
 Db 1 CCCAGGAGCAGCAGAAATTTCACCTGCTGTGAGCCCAATCCCTGGAGTCCAGAGG 60
 OY 374 TTTGAGCGTTGAGGTTACACTGCATGTCGAGCAAACTTCAGCGTCCCGTCTCAGCG 433
 Db 61 TTATGAGCATTTGAGGTTACACTGCATGTCGAGCAAACTTCAGCGTCCCGTCTCAGCG 120
 OY 434 CCCCCCAGCCCTCCAGAGATGCTCACCTTCACGTGTACATCCATAAGCGCTACC 493
 Db 121 CCCCCCAAGCCCTCCAGAGATGCTCACCTTCACGTGTACATCCATAAGCGCTACC 180
 OY 494 CCGAGCCCAAGCTGCTACTGATGATCAATAG-ACGACAACAGCCGTCGGACAGGCTC-T 551
 Db 181 CCAGGCCCAAGCTGCTACTGATGATCAATAGAGGACAACAGCATGTCGGACAGGCTCTT 240
 OY 552 GCAGATGACACCGCTCTTCTGAACATGCGGGCTTGATGACGTGTGTCACCGTCTGAG 611
 Db 241 GAAATGACACCGCTTTCTTGAACATGCGGGCTTGATGACGTGTGTCACCGTCTGAG 300
 OY 612 GATC-GCAGCAGCCCGCAGCGTGAACATGCTGCTGATGAGAACCTGCTTCTGAGC 670
 Db 301 GATGGGAACGAGCCCGCAGCGTGAACATGCTGCTGATGAGAACCTGCTTCTGAGC 360
 OY 671 AGAAGCTGCTGGCGCAGCAGAGAAATGACATGAGAGAGAGACAAAGATCAAG 730
 Db 361 ATTAAGTACTGTGGTATGAGAGAGAAATGACATGAGAGAGAGACAAAGATCAAG 420
 OY 731 AGAATCCAGTCAGTACCGCGAGAAAAA 758
 Db 421 AGAATCCAGTCAGTACCGCGAGAAAAA 448

RESULT 8

R23544
 LOCUS R23544 422 bp mRNA linear EST 20-APR-1995
 DEFINITION Yg34c12.11 Soares infant brain IN1B Homo sapiens cDNA clone
 IMAGE:34465 5', mRNA sequence.
 ACCESSION R23544
 VERSION R23544.1 GI:778432
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 422)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 M., Hultman, M., Kuwaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston
 R., Williamson, A., Woldman, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 CONTACT: Wilson RK
 JOURNAL Washington University School of Medicine
 COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 2783
 High quality sequence stops: 364 Source: IMAGE Consortium, LINT
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 2783 Std Error: 0.00
 Seq primer: M3RP1
 High quality sequence stop: 364.
 Location/Qualifiers
 1. 422

FEATURES
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 /db_xref="taxon:9606"
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 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="PH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: latmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAGAAATTCGCGCGCAGGAGAAATTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the latmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 100 a 122 c 121 g 78 t 1 others
 ORIGIN
 Query Match 42.2%; Score 365; DB 14; Length 422;
 Best Local Similarity 100.0%; Pred. No. 1.4e-89;
 Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 407 CAAACTTCAGCGCCGCTGTCAGCGCCGCCACAGACCCCTCCAGATGACTCACT 466
 Db 1 CAAACTTCAGCGCGCCGCTGTCAGCGCCGCCACAGACCCCTCCAGATGACTCACT 60
 OY 467 TCAGGTATCATTCATTAAGGCTACCCGACGCGCAACGCTGATGATCAATTAAGCAG 526
 Db 61 TCAGGTATCATTCATTAAGGCTACCCGACGCGCAACGCTGATGATCAATTAAGCAG 120
 OY 527 ACAACAGCCTGCTGGACAGCAGCTCTGCAGATGACACCGCTCTTGAACATCGGGGCT 586
 Db 121 ACAACAGCCTGCTGGACAGCAGCTCTGCAGATGACACCGCTCTTGAACATCGGGGCT 180
 OY 587 TGTATGACGTGGTACGCGTGTGAGATGCCAGAGACCCCGACGCTGAACATTGGCTGCT 646
 Db 181 TGTATGACGTGGTACGCGTGTGAGATGCCAGAGACCCCGACGCTGAACATTGGCTGCT 240

| | | |
|------------|--|-----|
| D6 | CATGCCCTGTGTTACAGGGCCCGT-----CCGAGGACGAGGAGCTCACCTTCAGCTGCAC | 117 |
| QY | 477 ATCCATAAAGCGGCTAACCCGACCACCTGTACTGATCATTAAGACGACACAGCCT | 536 |
| D6 | | |
| D6 | 118 GTCTACCAACGCGCTACCCGCGCCAAATGTGTACTGATCAACAAGACGACACAGCCT | 177 |
| QY | 537 GCTTGACCAAGGCTCTGACGAATGACACCCCTCTTCTTTGAACATCGCGGGCTTGTATGACGT | 596 |
| D6 | | |
| D6 | 178 GCTTGACAGCCCCCTGCAAGAATAACGCTGTCCCTGAACCGCGCGGCTGTATGATGT | 237 |
| QY | 597 GGTTACGCGTGTGAGATATCGACGAGACCCCGACGCGTGAACATTGGCTCTCATATGAGAA | 656 |
| D6 | | |
| D6 | 238 GGTGAGTGTCTGTAGAAATCGGGCGAACCCCGCATGTCAAAGTGGCTCTGTGATGAGAA | 297 |
| QY | 657 CGTCTTCTGTGACAGAACTGTACTGTGCGAGCCGACAGAGGAATGACATTCGAGAGAG | 716 |
| D6 | | |
| D6 | 298 TGTCTCTCTACACGAACTGTAC---GAGCGGCGACAGAAACGTTTCACGCGAACCAG | 354 |
| QY | 717 AGACAAGATCACAGAAATTCAGT-----CAGTACCGCGCGAGAAAACCGCGGCACGTG | 770 |
| D6 | | |
| D6 | 355 GGACAGAGCTTCACAGAGGACCCAGTGTGATGAGAGCCCACGCGGGAACACAGCAGGTTTT | 414 |
| QY | 771 GAGCATCTTGACTTCTGCTGTGCTGCTGTGTGATGCGTGGCGGTGACCATAGCTGGGTGTG | 830 |
| D6 | | |
| D6 | 415 TAGGCTCTTTCGCGTGTGCGCGGTGATGTGCTCTCTGGCTCTCGCCACGCGGTGCTGTG | 474 |
| QY | 831 CA 832 | |
| D6 | | |
| D6 | 475 CA 476 | |
| RESULT 10 | | |
| LOCUS | BI911468 | |
| DEFINITION | BI911468 771 bp mRNA linear .EST 16-OCT-2001 | |
| VERSION | 603063908F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5213400 5', | |
| KEYWORDS | mRNA sequence. | |
| SOURCE | BI911468 | |
| ORGANISM | BI911468.1 GI:16175218 | |
| REFERENCE | Homo sapiens | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| TITLE | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | |
| JOURNAL | NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) | |
| COMMENT | Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapds-femail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.lnll.gov Plate: LHAM1535 row: O column: 01 High quality sequence start: 19 High quality sequence stop: 414. Location/Qualifiers 1. 771 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5213400" /clone_1lb="NIH_MGC_118" /tissue_type="Leukocyte" /lab_host="DH10B" /note="Vector: pCMV-Sport6; site_1: NotI; site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for | |

Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenrto cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL: <http://genome-gsc.riken.go.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to

FEATURES

B-1 COUNT
ORIGIN

| | | |
|---------------------------|--------|----------------------------------|
| Best Local Similarity | 61.68; | Pred. No. 7.5e-26; |
| Matches 250; Conservative | 0; | Mismatches 150; Indels 5. Gaps 2 |

253 CTGATGTCACCGGGCCGGCAGTCTGCGGGCGACTTCTCCCTGGCGTGTTCACAGTCACC 312

Db 616 TCAAGATCTTGAAGAGGTGTCAGGCTGCCCTGTTGCACCAAACTT 661

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search completed: November 17, 2002, 05:26:42
Job time : 1257.62 secs
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QY 181 ACCGTTGAGTACCTACACATCCACAGAAACAGCTCTCTTGGAAAGGTGACAGCCGCTAC 240
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QY 241 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 300
Db 369 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 428
QY 301 TTCAACGTCACCCCGGAGAGCAGAGAAAGTTTCACTGCTGCTGGTGTGAGCCAACTCCCTG 360
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QY 361 GGATTCCAGAGGTTTGGAGCTTGGAGTTACATGATGATGAGCAAGCAACTTCAAGCTG 420
Db 489 GGATTCCAGAGGTTTGGAGCTTGGAGTTACATGATGATGAGCAAGCAACTTCAAGCTG 548
QY 421 CCGCTGTCAGCGCCCGCCACAGCCCTCCAGATGAGCTCACTTCACTGATACCC 480
Db 549 CCGCTGTCAGCGCCCGCCACAGCCCTCCAGATGAGCTCACTTCACTGATACCC 608
QY 481 ATAAAGGCTACCCCGAGCCCAAGGTACTGATCAATTAAGAGAGCAACAGCCGCTTG 540
Db 609 ATAAAGGCTACCCCGAGCCCAAGGTACTGATCAATTAAGAGAGCAACAGCCGCTTG 668
QY 541 GACCAAGCTCTGAGATGACACCGCTCTTCTTGAACATGCGGGGCTTGTATACGTGTC 600
Db 669 GACCAAGCTCTGAGATGACACCGCTCTTCTTGAACATGCGGGGCTTGTATACGTGTC 728
QY 601 ACCGTTGAGTACCTACAGAGAGCCCGGAGCCGTTGACATTTGCTGCTGCTAGAGAGCTG 660
Db 729 ACCGTTGAGTACCTACAGAGAGCCCGGAGCCGTTGACATTTGCTGCTGCTAGAGAGCTG 788
QY 661 CTTTGCAGCAGAACTGACTGCTGCGGAGCCGAGAGAAATGACATCGAGAGAGAGAC 720
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Db 849 AAGATCACAGAGATTCAGTACGACCGGCGAGAAAAAGCGGCGCCACGTGAGACATCTG 908
QY 781 GGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 909 GGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968
QY 841 TGCCTCAACACAGCTATGACAGT 864
Db 969 TGCCTCAACACAGCTATGACAGT 992

RESULT 2
; Sequence 64, Application us/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043p1
; CURRENT APPLICATION NUMBER: US/09/789,561
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: *PatentIn Ver. 2.0
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; SEQ ID NO 64
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: Homo sapiens
; us-09-789-561-64
Query Match 100.0%; Score 863.6; DB 10; Length 2751;
Best Local Similarity 99.9%; Pred. No. 3.3e-240;
Matches 863; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGGCTGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
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QY 61 CAGGAGAAAGAGTACAGACGATGGTAGGACGAGAGTGGAGCTGACGCTGCGCTG 120
Db 278 CAGGAGAAAGAGTACAGACGATGGTAGGACGAGAGTGGAGCTGACGCTGCGCTG 337
QY 121 GAAGGAGCCGTTTGGATTAAATGATGTTTACGATATATGGCAAAACAGTACGCGAAA 180
Db 338 GAAGGAGCCGTTTGGATTAAATGATGTTTACGATATATGGCAAAACAGTACGCGAAA 397
QY 181 ACCGTTGAGTACCTACACATCCACAGAAACAGCTCTTGGAAAGGTGACAGCCGCTAC 240
Db 398 ACCGTTGAGTACCTACACATCCACAGAAACAGCTCTTGGAAAGGTGACAGCCGCTAC 457
QY 241 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 300
Db 458 CGGAACCGAGCCCTGATGTACCGGCGGCGATGCTGCGGGGCGACTTCTCCCTGCGCTTG 517
QY 301 TTCAACGTCACCCCGGAGAGCAGAGAAAGTTTCACTGCTGCTGGTGTGAGCCAACTCC 360
Db 518 TTCAACGTCACCCCGGAGAGCAGAGAAAGTTTCACTGCTGCTGGTGTGAGCCAACTCC 577
QY 361 GGATTCCAGAGGTTTGGAGCTTGGAGTTTACATGATGATGAGCAAGCAACTTCAAGCCG 420
Db 578 GGATTCCAGAGGTTTGGAGCTTGGAGTTTACATGATGATGAGCAAGCAACTTCAAGCCG 637
QY 421 CCGCTGTCAGCGCCCGCCACAGCCCTCCAGATGAGCTCACTTCACTGCTGCTGCTGCTG 480
Db 638 CCGCTGTCAGCGCCCGCCACAGCCCTCCAGATGAGCTCACTTCACTGCTGCTGCTGCTG 697
QY 481 ATAAAGGCTACCCCGAGAGCAGAGAAAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 698 ATAAAGGCTACCCCGAGAGCAGAGAAAGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 757
QY 541 GACCAAGCTCTGAGATGACACCGCTCTTCTTGAACATGCGGGGCTTGTATACGTGTC 600
Db 758 GACCAAGCTCTGAGATGACACCGCTCTTCTTGAACATGCGGGGCTTGTATACGTGTC 817
QY 601 ACGTTGCTGAGATGCGACAGAGCCCGGAGCGTGAACATTGCTGCTGCTGCTGCTGCTGCTG 660
Db 818 ACGTTGCTGAGATGCGACAGAGCCCGGAGCGTGAACATTGCTGCTGCTGCTGCTGCTGCTG 877
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Db 878 CTTTGCAGCAGAACTGACTGCTGCGGAGCCGAGAGAAATGACATCGGAGAGAGAC 937
QY 721 AAGATCACAGAGATTCAGTACGACCGGCGAGAAAAAGCGGCGCCACGTGAGACATCTG 780
Db 938 AAGATCACAGAGATTCAGTACGACCGGCGAGAAAAAGCGGCGCCACGTGAGACATCTG 997
QY 781 GGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 998 GGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1057
QY 841 TGCCTCAACACAGCTATGACAGT 864
Db 1058 TGCCTCAACACAGCTATGACAGT 1081

RESULT 3
; us-09-764-853-210
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; Sequence 210, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 210
; LENGTH: 2616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-210

Query Match 99.8%; Score 862.4; DB 10; Length 2616;
Best Local Similarity 99.9%; Pred. No. 7,1e-240;

Matches 863; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 CAGGAGAAGAAAGTCAGAGCGATGTAGGCAAGGAGCTGAGCTGCGCTTGGCCT 120
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Db 184 CAGGAGAAGAAAGTCAGAGCGATGTAGGCAAGGAGCTGAGCTGCGCTTGGCCT 243

QY 121 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 180
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Db 244 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 303

QY 181 ACCGTGTGACCTTACCAATCCCAAGAACAGCTCTTGGAAAACTGGACGCCCTAC 240
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Db 304 ACCGTGTGACCTTACCAATCCCAAGAACAGCTCTTGGAAAACTGGACGCCCTAC 363

QY 241 CGGAACCGAGCCCTGATGTACCGCGCGGATGCTGGGGGCGACTTCCTGCGCTTG 300
    |||||||
Db 364 CGGAACCGAGCCCTGATGTACCGCGCGGATGCTGGGGGCGACTTCCTGCGCTTG 423

QY 301 TTCACGTCACCCGCCAGAGAGAGAGAGTTTCACTGCTGTGTGAGCCAACTCCCTG 360
    |||||||
Db 424 TTCACGTCACCCGCCAGAGAGAGAGAGTTTCACTGCTGTGTGAGCCAACTCCCTG 483

QY 361 GGATTCAGAGAGTTTGAAGCTTGAAGTTACACTGATGTGGCAGCAACTTCAAGCTG 420
    |||||||
Db 484 GGATTCAGAGAGTTTGAAGCTTGAAGTTACACTGATGTGGCAGCAACTTCAAGCTG 543

QY 421 CCGGTGTCAGCGCCGCCAGAGCCCTCCAGAGATGAGTCACTTCAAGTGAATCC 480
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QY 541 GACAGAGCTTGAAGATGACACCGCTTCTTGAACATGCGGGGCTTGTATGACGCTGCT 600
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Db 664 GACAGAGCTTGAAGATGACACCGCTTCTTGAACATGCGGGGCTTGTATGACGCTGCT 723

QY 601 AGCGTGTAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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QY 841 TGGCTCCAGACAGCTATGACAGT 864
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RESULT 4
US-09-764-853-390

; Sequence 390, Application US/09764853
; Patent No. US20020090672A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206

; CURRENT APPLICATION NUMBER: US/09/764,853
; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 390
; LENGTH: 2622

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-390

Query Match 99.8%; Score 862.4; DB 10; Length 2622;
Best Local Similarity 99.9%; Pred. No. 7,1e-240;

Matches 863; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 190 CAGGAGAAGAAAGTCAGAGCGATGTAGGCAAGGAGCTGAGCTGCGCTTGGCCT 249

QY 121 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 180
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Db 250 GAAGGAAGCCGTTTGAATTAATGATGTTACGTATATTGGCAACAGTGAAGTGA 309

QY 181 ACCGTGTGACCTTACCAATCCCAAGAACAGCTCTTGGAAAACTGGACAGCCCTAC 240
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QY 241 CGGAACCGAGCCCTGATGTACCGCGCGGATGCTGGGGGCGACTTCCTGCGCTTG 300
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Db 370 CGGAACCGAGCCCTGATGTACCGCGCGGATGCTGGGGGCGACTTCCTGCGCTTG 429

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QY 721 AAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US/09/978,295A
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/918585
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PRIORITY APPLICATION NUMBER: 60/085697

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[illegible]

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Db      810   GCCTGGTCGCCAACCCGCTGTGCAGCAGGA 840

RESULT 8
US-10-052-586--53
Sequence 53, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1CI
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088825
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088863
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089090
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 5.1%; Score 43.8; DB 12; Length 1998;
Best Local Similarity 47.0%; Pctd. No. 0.0053;
Matches 212; Conservative 0; Mismatches 227; Indels 12; Gaps 2;

QY 224 ACCTGACAGCCGCTACCGAACGAGCCCTGATGTCACCGCGCGGATGTCGCGGCGG 283
DB 402 ACCAGGCGAGCGGCTATGCGAACGCGCGCCCTCTCCCGGACCTGCTGGCAGAGGCA 461
QY 284 ACTTCTCCCTGGCGCTTGTTCACGTCACCCCGAGGACGAGAGAGATTCTACCTGCG 343
DB 462 AGCATCCCTGAGGCTGACGCGCGTGTGTGCGGAGGAGGAGGAGCTTACCTGCTTGC 521

QY 344 TGTGACCAATCCCTGGGATTCAGAGAGTTTGTGAGCTTGTACATGATGCTGG 403
DB 522 TGAGCATTCGGGATTCGGAGCGCTCGCTGACCTGACAGTGGCCGCTCCCA----- 576
QY 404 CAGCAACTTCAGGCGGCTGGTGCAGCGCCCCCAGAGCCCTCCAGATGAGCTCA 463
DB 577 -CTGGAAGCCAGCATACCTTGGAGCCCAAGAGACCTGCGGCCAGGGGACCGGTGA 635
QY 464 CCTTCAGGTACATTCATTAACGCTACCCAGGCCCAACGCTGTACTGTGATCAATAGA 523
DB 636 CCATCAGGTGGTCCAGTACAGAGGCTACCTGAGGCTGAGGTGCTGTGCGAGAGATGGGC 695
QY 524 CGGACAAACGCTCTGGAGCAGGCTCTGCAAGATGACACCGCTTCTTGAACATGCGGG 583
DB 696 AGGGGTGTGCCCTGTACGTGGCAAGCTGACCAAGTCGACAGATGGCC-----AACGAGCAGG 749
QY 584 GCTTGATGAGAGCGTGGTGTGAGGATCGCAGCGACCCCGCAGCGTGAACATTTGGCT 643
DB 750 GCTTGTTGATGTGCACAGCGTCTCTGCGGGTGTGTGCTGGGATGGCACTACAGCT 809
DB 644 GCTGCATAGAGAACGTCCTTCTGACAGAGAA 674
DB 810 GCTGTGGCGCAACCCGCTGCTGCAGCAGGA 840

RESULT 9
US-09-910-174A-27
; Sequence 27, Application US/09910174A
; Patent No. US20020106730A1
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174A
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-910-174A-27

Query Match 4.9%; Score 42.6; DB 10; Length 948;
Best Local Similarity 46.0%; Pred. No. 0.0084;
Matches 144; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 359 TGGGATTCAGAGAGTTTGTGACGTTGAGTTTACATGCTGACGAGCAACTTCAAGC 418
DB 371 TGAGCATTCAGAGACTTGTACAGCGTGTGTTAGCTGACGTGCCCCCTTACTGA 430
QY 419 TGCCCGTGTAGCGCCCCCAGAGCCCTCCAGAGATGAGCTCACTTCAAGTGTACAT 478
DB 431 AGCCAGATGACCTTGAAGCCCAAGAGACTTACGTCCAGGGAACATGTTGACATCA 490
QY 479 CCAATTAACGCTACCCAGGCCCAACGTTACTGATCAATTAAGAGGACAAACCCCTGC 538
DB 491 CGTGCTAGGTACAGGAGGTATTCGGAGGCCGAGGTGTTCTGGAAGATGAGAGGGAG 550
QY 539 TGGACAGGCTCTGCAAGATGACACCGCTCTTAAATATGCGGGCTTGTATGACGTGG 598
DB 551 TGCCCTTACGTGGCAATGTGACATCCAGATGGCCCAAGAGCGGGCTTGTGCTGTTG 610
QY 589 TCAGGCTGTGAGATGCGCAGGAGCCCGCAGGATGAACTTGGCTGCTGATGAGAGC 658
DB 611 ACAGGCTGTGAGGAGGTGCTGCTGAGGCTTAACGGACCTACAGCTCCCTGTTGAGCAACC 670

QY 659 TGCCTGTGCAGCA 671
DB 671 CGGTGTGACAGA 683

RESULT 10
US-09-910-174A-23
; Sequence 23, Application US/09910174A
; Patent No. US20020106730A1
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1el Members of the B7
; FILE REFERENCE: 35800/236924
; CURRENT APPLICATION NUMBER: US/09/910,174A
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-174A-23

Query Match 4.9%; Score 42.2; DB 10; Length 951;
Best Local Similarity 46.8%; Pred. No. 0.011;
Matches 211; Conservative 0; Mismatches 228; Indels 12; Gaps 2;

QY 224 ACGTGACAGCGCGCTACCGGAGCCCTGTGATGTACCGCGCGGATGCTGGCGGCG 283
DB 251 ACCAGGCGACGCGCTATGACCAACCGGAGCCCTCTTCCGAGACCTGTGACAGAGGCA 310
QY 284 ACTTCTCCCTGCGCTGTGTCAACGCTCAACCCCAAGAGCAGAGAGTTTCACTGCTGG 343
DB 311 ATGATCCTCTGAGGCTGACAGCGCTGCTGTGCGGAGGAGGAGCTTCACTGCTTGG 370
QY 344 TGTGACCAATCCCTGGGATTCAGAGAGTTTGTGACGTTGAGCTTACATGATGCTGG 403
DB 371 TGAGCATTCGGGATTCGGAGCGCTCGCTGACCTGACAGTGGCCGCTCCCTA----- 425
QY 404 CAGCAACTTCAGAGCGTCCCGCTGCTGACGCCCCCAGAGCCCTCCAGATGAGCTCA 463
DB 426 -CTGGAAGCCAGCATGACCTGTGAGGCCCAAGAGACTGCGGCCAGGGGACACGGTGA 484
QY 464 CCTTCAGGTGTACATTCATTAACGCTTACCCAGGCCCAACGTTTACTGTATCAATAGA 523
DB 485 CCATCAGGTGTCTCAGCTACAGGCTACCTTGAGGCTGAGGTGTTGTGCGAGAGTGGC 544
QY 524 CGGACAAACGCTGCTGACAGGCTGTGCAAGATGACACCGTCTTGAACATGCGGG 583
DB 545 AGGGTGTGCCCTTACTGAGCAAGCTGACACAGTGTGCAAGATGGCC-----AACGAGCAGG 598
QY 584 GCTTGATGAGCTGTGAGCGTGTGAGATGCGACGAGACCCCGAGCTGAACATTTGCT 643
DB 599 GCTTGTTGATGTGCACAGCGTCTCGCGGGTGTGCTGAGGCTGAAGTGGACCTTACAGCT 658
QY 644 GCTGCATAGAGAACGTCCTTCTGACAGAGAA 674
DB 659 GCTGTGTGCCCAACCCGCTGCTGCAGCAGGA 689

RESULT 11
US-09-875-338-8
; Sequence 8, Application US/09875338
; Patent No. US20020095024A1
; GENERAL INFORMATION:
; APPLICANT: MIKESSELL, GLEN E.
; APPLICANT: CHANG, HAN
; APPLICANT: FINGER, JOSHUA N.


```

; APPLICANT: YANG, GUICHEN
; APPLICANT: LU, PIN
; APPLICANT: ZHOU, XIA-DI
; APPLICANT: PEACH, ROBERT
; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
; FILE REFERENCE: 3053-4071US2
; CURRENT APPLICATION NUMBER: 60/272,107
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,811
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Artificial Sequence
; SEQUENCE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Fusion construct
US-09-728-421d-11.rnpb

```

Query Match 4.9%; Score 42.2; DB 10; Length 2097;

Best Local Similarity 46.8%; Pred. No. 0.016; Mismatches 228; Indels 12; Gaps 2;

```

Matches 211; Conservative 0; Mismatches 228; Indels 12; Gaps 2;
QY 224 ACCTGACAGCCGCTACCGAACCGAGCCCTGATGTCACCGCGCGGATGTCGCGGCGG 283
  || || || || || || || || || || || || || || || || || || || || || ||
DB 251 ACCAGGCGAGCGGCTATGCGCAACCGAGCCGCTCTCCGGAGCTGCGGACAGAGGCA 310
  || || || || || || || || || || || || || || || || || || || || || ||
QY 284 ACTTCTCCCTGCGCTGTTTCACAGCTACCCGCCAGAGAGAGAGAGAGAGAGAGAGAG 343
  || || || || || || || || || || || || || || || || || || || || || ||
DB 311 ACAGCATCCCTGAGGCTGAGCGGCTGCTGTGGCGGAGAGAGAGAGAGAGAGAGAGAG 370
  || || || || || || || || || || || || || || || || || || || || || ||
QY 344 TGTGAGCAATCCCTGAGGATTCAGAGAGGTTTGTGAGCTGTGATGATGATGATGATG 403
  || || || || || || || || || || || || || || || || || || || || || ||
DB 371 TGAGCATCCCGGATTTGCGAGAGCGCTGCGCTGACCTGAGAGTGCGCCCTCCCTA---- 425
  || || || || || || || || || || || || || || || || || || || || || ||
QY 404 CAGCAAACTTCAAGCGTGCCTGCTCAGCGCCGCCGCCAGAGCCCTCCAGAGATGAGCTGA 463
  || || || || || || || || || || || || || || || || || || || || || ||
DB 426 -CTGGAAGCCAGAGATGAGCTGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 484
  || || || || || || || || || || || || || || || || || || || || || ||
QY 464 CCTTCACTGCTATCATCAATCAAGAGGCTACCCAGCGCCCAAGCTGTACTGATCAATAA 523
  || || || || || || || || || || || || || || || || || || || || || ||
DB 485 CCATCACTGCTGCTCAAGCTACAGAGGCTACCTGAGGCTGAGGCTGTGAGAGAGAGAG 544
  || || || || || || || || || || || || || || || || || || || || || ||
QY 524 CGAGCAAGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
  || || || || || || || || || || || || || || || || || || || || || ||
DB 545 AGGCTGCTGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598
  || || || || || || || || || || || || || || || || || || || || || ||
QY 584 GCTTGTATGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
  || || || || || || || || || || || || || || || || || || || || || ||
DB 599 GCTTGTATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 658
  || || || || || || || || || || || || || || || || || || || || || ||
QY 644 GCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 674
  || || || || || || || || || || || || || || || || || || || || || ||
DB 659 GCCTGCTGCGCAACCCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
  || || || || || || || || || || || || || || || || || || || || || ||

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RESULT 12
US-09-728-421d-11.rnpb

; Sequence 6, Application US/09875338

; Patent No. US20020095024A1

; GENERAL INFORMATION:

; APPLICANT: MIKESSEL, GLEN E.

; APPLICANT: CHANG, HAN

; APPLICANT: FINGER, JOSHUA N.

; APPLICANT: YANG, GUICHEN

; APPLICANT: LU, PIN

; APPLICANT: ZHOU, XIA-DI

; APPLICANT: PEACH, ROBERT

```

; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
; FILE REFERENCE: 3053-4071US2
; CURRENT APPLICATION NUMBER: 60/272,107
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,811
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3197
; TYPE: DNA
; ORGANISM: Homo sapiens
; SEQUENCE:
; OTHER INFORMATION:
US-09-728-421d-11.rnpb

```

Query Match 4.9%; Score 42.2; DB 10; Length 3197;

Best Local Similarity 46.8%; Pred. No. 0.019; Mismatches 228; Indels 12; Gaps 2;

Matches 211; Conservative 0; Mismatches 228; Indels 12; Gaps 2;

```

QY 224 ACCTGACAGCCGCTACCGAACCGAGCCCTGATGTCACCGCGCGGATGTCGCGGCGG 283
  || || || || || || || || || || || || || || || || || || || || || ||
DB 371 ACCAGGCGAGCGGCTATGCGCAACCGAGCCGCTCTCCGGAGCTGCGGACAGAGGCA 430
  || || || || || || || || || || || || || || || || || || || || || ||
QY 284 ACTTCTCCCTGCGCTGTTTCACAGCTACCCGCCAGAGAGAGAGAGAGAGAGAGAGAG 343
  || || || || || || || || || || || || || || || || || || || || || ||
DB 431 ACAGCATCCCTGAGGCTGAGCGGCTGCTGTGGCGGAGAGAGAGAGAGAGAGAGAGAG 490
  || || || || || || || || || || || || || || || || || || || || || ||
QY 344 TGTGAGCAATCCCTGAGGATTCAGAGAGGTTTGTGAGCTGTGATGATGATGATGATG 403
  || || || || || || || || || || || || || || || || || || || || || ||
DB 491 TGAGCATCCCGGATTTGCGAGAGCGCTGCGCTGACCTGAGAGTGCGCCCTCCCTA---- 545
  || || || || || || || || || || || || || || || || || || || || || ||
QY 404 CAGCAAACTTCAAGCGTGCCTGCTCAGCGCCGCCGCCAGAGCCCTCCAGAGATGAGCTGA 463
  || || || || || || || || || || || || || || || || || || || || || ||
DB 546 -CTGGAAGCCAGAGATGAGCTGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 604
  || || || || || || || || || || || || || || || || || || || || || ||
QY 464 CCTTCACTGCTATCATCAATCAAGAGGCTACCCAGCGCCCAAGCTGTACTGATCAATAA 523
  || || || || || || || || || || || || || || || || || || || || || ||
DB 605 CCATCACTGCTGCTCAAGCTACAGAGGCTACCTGAGGCTGAGGCTGTGAGAGAGAGAG 664
  || || || || || || || || || || || || || || || || || || || || || ||
QY 524 CGAGCAAGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
  || || || || || || || || || || || || || || || || || || || || || ||
DB 665 AGGCTGCTGCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 718
  || || || || || || || || || || || || || || || || || || || || || ||
QY 584 GCTTGTATGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
  || || || || || || || || || || || || || || || || || || || || || ||
DB 719 GCTTGTATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 778
  || || || || || || || || || || || || || || || || || || || || || ||
QY 644 GCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 674
  || || || || || || || || || || || || || || || || || || || || || ||
DB 779 GCCTGCTGCGCAACCCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 809
  || || || || || || || || || || || || || || || || || || || || || ||

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RESULT 13
US-09-728-421d-11.rnpb

; Sequence 19, Application US/09875338

; Patent No. US20020095024A1

; GENERAL INFORMATION:

; APPLICANT: MIKESSEL, GLEN E.

; APPLICANT: CHANG, HAN

; APPLICANT: FINGER, JOSHUA N.

; APPLICANT: YANG, GUICHEN

; APPLICANT: LU, PIN

; APPLICANT: ZHOU, XIA-DI

; APPLICANT: PEACH, ROBERT

; TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR

; FILE REFERENCE: 3053-4071US2

; CURRENT APPLICATION NUMBER: 60/272,107

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/209,811

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: 60/272,107

```
; PRIOR APPLICATION NUMBER: 60/209, 811
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-338-19

Query Match
Best Local Similarity 4.9%; Score 42.2; DB 10; Length 3197;
Matches 211; Conservative 0; Mismatches 228; Indels 12; Gaps 2;

OY 224 AGGTGACGACCGCTTACCGGACCGACCGCTGATGTCACCGGCGGACGCTGCGGGGCG 283
DB 371 ACCAGGGCAGCGCTTATGCCAACCGCAGCGCCCTTCTCCCGGACCTGCGGACAGGGCA 430
OY 284 ACTTCTCCCTGCGCTTGTTCACGCTCACCCCGAGGACGACGAGATTTCACCTGCTGG 343
DB 431 ACGCATCCCTGAGGGCTGCAAGCGGCTGCTGTGGCGGACGAGGCGACCTTCACTGCTTG 490
OY 344 TGTGAGCCCAATCCCTGGGATTCAGAGAGTTTGAAGCTTGAAGTTACACTGATGTG 403
DB 491 TTAGCATCCGGGATTTCCGAGCGCTGCGCTAGCCTGCAAGGTGGCCCTCA----- 545
OY 404 CAGCAACTTCAAGCGCTGCGCTGCTGAGCGCCCGCCACAGCCCTTCCAGATGAGCTCA 463
DB 546 -CTCGAAGCCCGACATGACCTTGTGAGCCCAACAGAGACCTTCCGCGGACAGGAGTGA 604
OY 464 CCTTCACGTGTACATTCATTAACGGCTACCCCGAGCCCAACGTTGATGATCAATAGA 533
DB 605 CCATCAGCGTCTCCAGCTACAGGGGCTACCTGAGGCTGAGTGTCTGCGAGATGGCG 664
OY 524 CGGACAACAGCCGCTGGAGCCAGGCTCTGAGATGACACCGCTCTTGAATGCGG 583
DB 665 AGGCTGTGCCCTGACTGCGACGTGACACGCTGCGAGATGGCC-----AACGACAGG 718
OY 584 GCTTGTATGACGTGTGACGCTGCTGAGATGCGACGAGACCCCGACCGTGAATGGCT 643
DB 719 GCTTGTATGATGTGACACATCTCTCGGCTGTGCTGGTGTGAATGCGACCTAGACGT 778
OY 644 GCTGCTAGAGAACGCTTCTTGCACAGAA 674
DB 779 GCGTGTGCGCAACCCCGCTGCTGCACAGGA 809

RESULT 14
US-09-875-338-10
Patent No. US20020095024A1
GENERAL INFORMATION:
APPLICANT: MIKESELL, GLEN E.
APPLICANT: CHANG, HAN
APPLICANT: FINGER, JOSHUA N.
APPLICANT: YANG, GUCHEN
APPLICANT: LU, PIN
APPLICANT: ZHOU, XIA-DI
APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
FILE REFERENCE: 3053-4071052
CURRENT APPLICATION NUMBER: US/09/875,338
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/272,107
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/209,811
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 951
TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-875-338-10

Query Match
Best Local Similarity 4.7%; Score 40.2; DB 10; Length 951;
Matches 212; Conservative 0; Mismatches 228; Indels 15; Gaps 2;

OY 229 GACAGCCGCTACCGGAACCGCCGTGATGTCAACCGCGCGCATGCTGCGGGCGACTTC 288
DB 241 GAAGGCCGGGACCGAGGCGACCTATGCCAACCGCAGCGCCCTTCCCGGACCTGCTG 300
OY 289 TCCCTGCGCTTGTTCACGCTCACCCCGAGGACGACGAGATTTCACCTGCTGTTG 348
DB 301 GCACAAGCCAAATCATCTCTGAGGCTGACGCGGCTGCTGTGCGGACGAGGCGACACTTC 360
OY 349 AGCCATCCCTGGGATTCAGAGAGTTTGAAGCTTGAAGTTACTGCTATGCGGAC-- 406
DB 361 ACCTGCTTGTGAGCATCCCGGATTTCCGACGCGCTGCTGAGCTGCAAGGTGGCGCT 420
OY 407 -----CAAACTTCAAGCGCTGCTGCTGAGCGCCCGCCACAGCCCTTCCAGATGAG 459
DB 421 CCTACTCGAAGCCGACATGACCTGAGGCCCAACAGAGACCTGCGGCGGACGACG 480
OY 460 CTCACCTTCACTGTATCATCAATCAAAAGGCTACCCCGAGCGCAAGTGTACTGATCAAT 519
DB 481 GTGACCATCACTGTCTCAAGCTACCGGGGCTACCTGAGGCTGAGGTGTTCTGCGAGGAT 540
OY 520 AAGAGGACACAGCCCTGCTGGAGCCAGGCTCTGCAATGACACGCTTCTTGAACATG 579
DB 541 GGGCAGGGGTGTGCCCTGACTGCGCAAGTGACCAAGCTCGCAGATGCC-----AACGAG 594
OY 580 CGGGCTTGTATGACGTGTGTCAGCGTGTGAGATGCGACGAGACCCCGAGCTGAACATT 639
DB 595 CAGGCTTGTATTGATGTGACACAGCTGCTGCGGCTGTGCTGCTGCTGCTGCTGCTGCT 654
OY 640 GGTGCTGCTAGAGAACGCTTCTTGCACAGAA 674
DB 655 AGCTGCTGTGTGCGCAACCCCGCTGCTGCACAGGA 689

RESULT 15
US-09-789-561-12
Sequence 12, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: P2043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 3436
TYPE: DNA
ORGANISM: Homo sapiens
US-09-789-561-12

Query Match
Best Local Similarity 4.7%; Score 40.2; DB 10; Length 3436;
Matches 212; Conservative 0; Mismatches 228; Indels 15; Gaps 2;

OY 229 GACAGCCGCTACCGGAACCGCCGTGATGTCAACCGCGCGCATGCTGCGGGCGACTTC 288
DB 1042 GAAGGCCGGGACCGAGGCGGCTATGCGCAACCGCAGCGCCCTTCTCCCGGACCTGCTG 1101
OY 289 TCCCTGCGCTTGTTCACGCTCACCCCGAGGACGACGAGATTTCACCTGCTGTTG 348
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Db 1102 GCACAGGCAATGCATCCCTGAGGCTGAGGCGCTGCGTGTGCGGACGAGGGCAGCTTC 1161
OY 349 AGCCAAATCCCTGGGATTTCCAGAGGTTTTCAGCTGTGAGGTTTACATGCAATGTGGCAG-- 406
Db 1162 ACCTGCTTCGTGAGCATCCGGGATTTGGCAGCGCTGCTCCGTCAAGCTGTGAGGTGGCCGCT 1221
OY 407 -----CAAACTTCAGCGGTGCGGTGTCAAGCGCCGCCACAGCCCTTCCAGATGAG 459
Db 1222 CCTTACTGGAAGCCCAAGCATGACCTGTGAGCCCAACAAAGGACCTGCGGCGCAGGGGACAG 1281
OY 460 CTCACCTTCAGGTGTACATCCATTAACGGCTACCCAGGCCCCAAGCTGTACTGTGATCAAT 1281
Db 1282 GTGACCATCAAGTGTCTCAGCTTACCGGGCTTACCTGTGAGGCTGAGGTGTCTGTGCAAGAT 1341
OY 520 AAGACGGACAACAGCTGTGAGGACCAAGGCTGTGAGATGACACCGTCTTGTGAACATG 1341
Db 1342 GGGCAGGGGTGCGCCCTGACTGGCAAGTGACGACGTCGAGATGCGC-----AACGAG 1395
OY 580 CGGGGCTTGTATGAGGTGTGACGCTGTGAGGATGSCACGAGACCCCGCAGCGTGAACATT 639
Db 1396 CAGGGCTTGTGTATGTGACGACGCTCTGCGGTGTGTGTGCTGTGCGAATGCGACCTTAC 1455
OY 640 GGCTGCTGCATAGAGAACGTGCTTGTGACAGAGAA 674
Db 1456 AGCTGCTGTGTGCGCAACCCCGTGTGACAGAGA 1490
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Search completed: November 17, 2002, 06:45:06
Job time : 45.2984 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 17, 2002, 03:10:15 ; Search time 35.882 Seconds
(without alignments)
7384.454 Million cell updates/sec

Title: US-09-728-421D-11

Perfect score: 864
Sequence: 1 atgcggctggcagctctg.....tccacacagctatgcaggt 864

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs, 15338381 residues

T number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1na/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/1na/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/1na/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/1na/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/1na/PCrUS.COMB.seq.*
6: /cgn2_6/ptodata/1/1na/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 4 | 43.4 | 5.0 | 3468 | 3 US-08-459-504B-2 | Sequence 2, Appl1 |
| 5 | 43.4 | 5.0 | 3468 | 3 US-08-459-444-2 | Sequence 2, Appl1 |
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| 41 | 37.6 | 4.4 | 4403765 | 4 US-09-103-840A-2 | Sequence 2, Appl1 |
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ALIGNMENTS

RESULT 1
US-07-951-715A-2
Sequence 2, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rochstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CCG 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..3468
; OTHER INFORMATION: /product= "Full-length pure maize
; OTHER INFORMATION: optimized synthetic Bt"
; OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn11.mze"
US-07-951-715A-2

Query Match          5.0%; Score 43.4; DB 1; Length 3468;
Best Local Similarity 46.3%; Pred. No. 0.035;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

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RESULT 2
US-08-459-448A-2
Sequence 2, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Ewola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlino, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttle, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains

STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentm Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..3468
OTHER INFORMATION: /product= "Full-length pure maize
OTHER INFORMATION: optimized synthetic Bt"
OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn11.mze"
US-08-459-448A-2

Query Match          5.0%; Score 43.4; DB 2; Length 3468;
Best Local Similarity 46.3%; Pred. No. 0.035;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

195 CCACATCCCAAGACAGCTCTCTGGAAAGAGTGACAGCGCGTACCGGAGACGCCCT 254
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Db 1125 CAACAACACAGAGCTGAGCGCTGAGAGCGGACCGAGTTCGCTACGACAGCA 1184

QY 255 GATGTCAACGGCGCGGACAGTGTGCGGCGGAGCTTCTCCCTGGCTTCAACGTCACCC 314
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QY 315 CCAGAGAGAGCAGAAGTTTCACTGCTGTGTGAGCCAAATCCGTGGAGTTCCAGAGGT 374
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Db 1245 CCAGAGACAAACAGTGCCTCCCGCCGAGGGCTTCAGCCACCGCTGAGCCAGTGAAT 1304

QY 375 TTGTAGCGTTAGGTTACATGCTATGTGGCAGCAAACTTCAGCGTCCCGCTGCAGAGCG 434
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Db 1425 CCGACCAA 1433
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US-08-459,595A-2
: Sequence 2, Application US/08459595A
: Patent No. 6018104
: GENERAL INFORMATION:
: APPLICANT: Kozielec, Michael G.
: APPLICANT: Desai, Nalini M.
: APPLICANT: Lewis, Kelly S.
: APPLICANT: Kramer, Vance C.
: APPLICANT: Warren, Gregory W.
: APPLICANT: Evola, Stephen V.
: APPLICANT: Crossland, Kyle D.
: APPLICANT: Wright, Martha S.
: APPLICANT: Merlino, Ellis J.
: APPLICANT: Launis, Karen L.
: APPLICANT: Rothstein, Steven J.
: APPLICANT: Bowman, Cindy G.
: APPLICANT: Dawson, John L.
: APPLICANT: Dunder, Erik M.
: APPLICANT: Pace, Gary M.
: APPLICANT: Suttie, Janet L.
: TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
: TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6018104artis Corporation
: STREET: Patent & Trademark Dept., 520 White Plains
: STREET: Rd., POB 2005
: CITY: Tarrytown
: STATE: New York
: COUNTRY: USA
: ZIP: 10591-9005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,595A
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/951,715
: FILING DATE: 25-SEP-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/772,027
: FILING DATE: 04-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Pace, Gary M.
: REGISTRATION NUMBER: 40403
: REFERENCE/DOCKET NUMBER: CGC 1577/CIF/DIV3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8582
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3468 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "Synthetic DNA"
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: 1..3468
: OTHER INFORMATION: /product="Full-length pure maize
: OTHER INFORMATION: optimized synthetic Bt"
: OTHER INFORMATION: /note="Disclosed in Figure 3 as syn17.mze"
US-08-459,595A-2
Query Match 5.0%; Score 43.4; DB 3; Length 3468;
Best Local Similarity 46.3%; Pred. No. 0.035;

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Matches 143: Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 195 CCACATCCCAAGACAGACTCTCTTGAAAAACGTGACACAGCCGCTACCGAACCAGCCCT 254
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Db 1305 GTTCCGCGACGGCTTCACCAACAGCAGCGGTGAGCATCATCCGCGCCCATGTTCAGCGT 1364
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QY 435 CCCCCACAGCCCTTCCACGATGAGCTACCTTCACGTGTACATTCATTAACGCGTACC 494
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Db 1365 GATCCACCGCAGCGCGGATTTCACACATCATCTCCCGACAGCCAGATTCACCAAGATCC 1424
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      |||||
Db 1425 CCTGACCA 1433

RESULT 4
US-08-459-504B-2
: Sequence 2, Application US/08459504B
: Patent No. 6075185
: GENERAL INFORMATION:
: APPLICANT: Koziel, Michael G.
: APPLICANT: Desai, Naini M.
: APPLICANT: Lewis, Kelly S.
: APPLICANT: Kramer, Vance C.
: APPLICANT: Warren, Gregory W.
: APPLICANT: Evola, Stephen V.
: APPLICANT: Crossland, Lyle D.
: APPLICANT: Wright, Martha S.
: APPLICANT: Merlin, Ellis J.
: APPLICANT: Launis, Karen L.
: APPLICANT: Rothstein, Steven J.
: APPLICANT: Bowman, Cindy G.
: APPLICANT: Dawson, John L.
: APPLICANT: Dunder, Erik M.
: APPLICANT: Pace, Gary M.
: APPLICANT: Suttie, Janet L.
: TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
: TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6075185artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,504B
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/459,595
: FILING DATE: 02-JUN-1995
: APPLICATION NUMBER: US 07/951,715
: FILING DATE: 25-SEP-1992
: PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..3468
OTHER INFORMATION: /product= "Full-length pure maize
OTHER INFORMATION: optimized synthetic Bt"
OTHER INFORMATION: /note= "Disclosed in Figure 3 as syn1T.mze"
US-08-459-504B-2

Query Match 5.0%; Score 43.4; DB 3; Length 3468;
Best Local Similarity 46.3%; Pred. No. 0.035;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 195 CCACATCCCAAGAGACAGTCTCTTGAAAGGTGACAGCGGCTACCGAAGCGAGCCCT 254
DB 1125 CACAAACACAGACAGTCTCTTGAAAGGTGACAGCGGCTACCGAAGCGAGCCCT 1184
QY 255 GATGTACCGCGCGGCGATGCTGCGGGCGGACTTCTCCCTGCTTGTCAAGTCAAGCC 314
DB 1185 CCGCCCAAGCGCGGCGATGCTGCGGGCGGACTTCTCCCTGCTTGTCAAGTCAAGCC 1244
QY 315 CCAGAGACAGCAAGTTTACTGCTGCTGCTTGTGAGCCCAATCCCTGGATTCCAGAGGT 374
DB 1245 CCAGAACACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1304
QY 375 TTGAGCGTTGAGTTACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 434
DB 1305 GTTCGCGAGCGGCTGCAAGACAGCGGCTGAGCATCATCCGCGCCCATGTTCAAGCTG 1364
QY 435 CCCCACAGCGCCCTCCAGATGATGCTACCTTCAGCTGATCATCATTAACGGCTACCC 494
DB 1365 GATCCACGCGAGCGCGAGTTCAACAACATCATCTCCAGCAGCCAGATCAACCGATCC 1424
495 CAGGCCCAA 503
DB 1425 CCGAGCCAA 1433

RESULT 5
US-08-459-444-2
Sequence 2, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/PI/CGC1577/CIP/DIV6

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3468 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Synthetic DNA"

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: misc.feature

LOCATION: 1..3468

OTHER INFORMATION: /product= "Full-length pure maize

optimized synthetic Bt"

/note= "Disclosed in Figure 3 as syn1T.mze"

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-459-444-2

Query Match 5.0%; Score 43.4; DB 3; Length 3468;

Best Local Similarity 46.3%; Pred. No. 0.035;

Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 195 CCACATCCCAAGAGACAGTCTCTTGAAAGGTGACAGCGGCTACCGAAGCGAGCCCT 254
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495 CAGGCCCAA 503
DB 1425 CCGAGCCAA 1433

7
RESULT 6
US-09-053-549-3
; Sequence 3, Application US/09053549
; Patent No. 6121521
; GENERAL INFORMATION:
; APPLICANT: Desai, Nallini
; TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121521artls Corporation
; STREET: 3054 Cornwallis Rd
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,549
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Page, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8682
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..3468
; OTHER INFORMATION: /product= "Full-length pure maize
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; NAME/KEY: CDS
; LOCATION: 1..3465
; US-09-053-549-3
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Best Local Similarity 46.3%; Pred. No. 0.035;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
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DB 1185 CTTGCCAGCGCGCTGTACCGACAGACGCGACCTGTGACACCTGTGACAGATCCCCC 1244
QY 315 CCAGAGCAGAGAAATTTCACTGCTGTGTTGAGCCAAATCCCTGGGATTCACAGAGT 374
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DB 1365 GATCCACCCGAGCGCGAGTTCAACATCATCTCCAGCAGCAGATCACCAGATCCC 1424
QY 495 CAGGCCCAA 503
DB 1425 CCGTACCAA 1433
RESULT 7
US-09-547-422-2
; Sequence 2, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Kozel, Michael G.
; Desai, Nallini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artls Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-APR-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3468 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..3468
; OTHER INFORMATION: /product= "Full-length pure maize
; optimized synthetic Bt"
; /note= "Disclosed in Figure 3 as syn1T.mze"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-547-422-2

APPLICANT: Mullins, Martha A
 APPLICANT: Nye, Gordon J
 APPLICANT: Carr, Brian
 APPLICANT: Desai, Nalini M
 APPLICANT: Kostichka, N. Kristy
 APPLICANT: Duck, Nicholas B
 APPLICANT: Estuch, Juan J
 TITLE OF INVENTION: A No. 5877012el Class of Proteins for the
 TITLE OF INVENTION: Control of Plant Pests
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.308
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,219B
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/463,483
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/314,594
 FILING DATE: 09-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/218,018
 FILING DATE: 23-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/037,057
 FILING DATE: 25-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Garry M.
 REGISTRATION NUMBER: 40,403
 REFERENCE/DOCKET NUMBER: CGC 1925
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8582
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2241 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic DNA encoding
 DESCRIPTION: VIP3A(c)"
 HYPOTHETICAL: NO
 US-08-838-219B-20

| Query Match | 4.7% | Score 40.2 | DB 2 | Length 2241 |
|-----------------------|--|----------------|----------------|-------------|
| Best Local Similarity | 45.6% | Pred. No. 0.21 | | |
| Matches 141 | Conservative | 0 | Mismatches 168 | Indels |
| | | | Gaps | 0 |
| QY | 425 TCGTAGCGCCCGCCACAGCCCTTCCAGATGATGACCTTCACCTGTATACATCCATAA | 484 | | |
| | | | | |
| Db | 731 TCGCGCCGACGGCCCTGTGAAGACCGCCAGCAGCTATATCCCAAGGAAACGTGAAGACA | 790 | | |
| QY | 485 ACGGCTACCCGACAGGCCACGCTGTATGATCATTAAGACGGACAACGCTGTGGACC | 544 | | |
| | | | | |
| Db | 791 GCGGACGAGAGGTGGGCAACGTTGTACACTTCTGTATGCTGTGACGCCCTGCAGGCC | 850 | | |
| QY | 545 AGGCTCTGCAGATGACACCGTCTTCTTGAAATCGCGGGCGTTGTATGACGTGGTCAGG | 604 | | |
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| Db | 851 AGGCGTTCCTGACCCCTGTGACCCCTGTGCAACGCTCTGCGCTTGGCGACATCGACTATA | 910 | | |

[illegible]

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1 RESULT 13
2 US-09-233-336A-20
3 Sequence 20, Application US/09233336A
4 Patent No. 6107279
5 GENERAL INFORMATION:
6 APPLICANT: Warren, Gregory W
7 APPLICANT: Koziel, Michael G
8 APPLICANT: Mullins, Martha A
9 APPLICANT: Nye, Gordon J
10 APPLICANT: Carr, Brian
11 APPLICANT: Desai, Nalini M
12 APPLICANT: Kostichka, N. Kristy
13 APPLICANT: Duck, Nicholas B
14 APPLICANT: Estruch, Juan J
15 TITLE OF INVENTION: A No. 6107279el Class of Proteins for the
16 TITLE OF INVENTION: Control of Plant Pests
17 NUMBER OF SEQUENCES: 20
18 CORRESPONDENCE ADDRESS:
19 ADDRESSEE: CIBA-GEIGY Corporation
20 STREET: 7 Skyline Drive
21 CITY: Hawthorne
22 STATE: NY
23 COUNTRY: USA
24 ZIP: 10532
25 COMPUTER READABLE FORM:
26 MEDIUM TYPE: Floppy disk
27 COMPUTER: IBM PC compatible
28 OPERATING SYSTEM: PC-DOS/MS-DOS
29 SOFTWARE: Patentin Release #1.0, Version #1.30B
30 CURRENT APPLICATION DATA:
31 APPLICATION NUMBER: US/09/233,336A
32 FILING DATE:
33 CLASSIFICATION:
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: 08/838,219
36 FILING DATE:
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 08/314,594
39 FILING DATE: 09-SEP-1994
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 08/218,018
42 FILING DATE: 23-MAR-1994
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: US 08/037,057
45 FILING DATE: 25-MAR-1993
46 ATTORNEY/AGENT INFORMATION:
47 NAME: Pace, Gary M.
48 REGISTRATION NUMBER: 40,403
49 REFERENCE/DOCKET NUMBER: CGC 1925
50 TELECOMMUNICATION INFORMATION:
51 TELEPHONE: 919-541-8582
52 TELEFAX: 919-541-8689
53 INFORMATION FOR SEQ ID NO: 20:
54 SEQUENCE CHARACTERISTICS:
55 LENGTH: 2241 base pairs
56 TYPE: nucleic acid
57 STRANDEDNESS: single
58 TOPOLOGY: linear
59 MOLECULE TYPE: other nucleic acid
60 DESCRIPTION: /desc = "synthetic DNA encoding

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DESCRIPTION: VIP3A(c)⁺
HYPOTHETICAL: NO
US-09-233-336A-20

Query Match
Best Local Similarity 45.6%; Score 40.2; DB 3; Length 2241;
Matches 141; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

425 TCGTCAGCGCCGCCACAGCCCTCCAGAGTACGCTTACGCTGATCCATAA 484
DB 731 TCGCGCCGACGCGCCCTGAGACCGGACGAGCTGATCACCAGAGAGAGTGAAGCA 790
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QY 545 AGGCTCTGCAAGATGACACCGCTCTTGTGAACATGCGGGGCTGTATGAGTGGTGCAG 604
DB 851 AGGCTCTTCTGACCGCTGACCGCTCTGTCGCAAGCTGCTGGGCTGGCCGACATGCACTACA 910
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QY 725 TCACAGAGA 733
DB 1031 ACGCCAAAGA 1039

RESULT 14
US-09-233-752A-20
Sequence 20, Application US/09233752A
Patent No. 6137033
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalin M
APPLICANT: Koslichka, N. Kristy
APPLICANT: Duck, Nicholas B
TITLE OF INVENTION: A No. 6137033el Class of Proteins for the
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,752A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,219
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1925
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2241 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA encoding
DESCRIPTION: VIP3A(c)⁺
HYPOTHETICAL: NO
US-09-233-752A-20

Query Match
Best Local Similarity 45.6%; Score 40.2; DB 3; Length 2241;
Matches 141; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

425 TCGTCAGCGCCGCCACAGCCCTCCAGAGTACGCTTACGCTGATCCATAA 484
DB 731 TCGCGCCGACGCGCCCTGAGACCGGACGAGCTGATCACCAGAGAGAGTGAAGCA 790
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DB 971 CGACCTTGACCAACCTTGACCAACCCGAACTACGCCAAGTGAAGGCGACGACGAGG 1030
QY 725 TCACAGAGA 733
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RESULT 15
US-09-402-036-20
Sequence 20, Application US/09402036
Patent No. 6291156
GENERAL INFORMATION:
APPLICANT: Estruch, Juan J.
APPLICANT: Yu, Cao-Guo
APPLICANT: Warren, Gregory W.
APPLICANT: Desai, Nalin M
APPLICANT: Koziel, Michael
TITLE OF INVENTION: Plant Pest Control
FILE REFERENCE: S-21284C
CURRENT APPLICATION NUMBER: US/09/402,036
FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: PCT/EP98/01952
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 08/838,219
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,263

/ PRIOR FILING DATE: 1997-04-03
/ PRIOR APPLICATION NUMBER: 08/832,265
/ PRIOR FILING DATE: 1997-04-03
/ PRIOR APPLICATION NUMBER: 08/463,483
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: 08/314,594
/ PRIOR FILING DATE: 1994-09-09
/ PRIOR APPLICATION NUMBER: 08/218,018
/ PRIOR FILING DATE: 1994-03-24
/ PRIOR APPLICATION NUMBER: 08/037,057
/ PRIOR FILING DATE: 1993-03-25
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 2241
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
/ OTHER INFORMATION: encoding VIP3A(c)
/ 09-402-036-20

Query Match 4.7%; Score 40.2; DB 4; Length 2241;
Best Local Similarity 45.6%; Pred. No. 0.21;
Matches 141; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

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QY 665 TGCAGCAGAACTGACTGTGCGAGCCAGACAGAAATGACATCGAGAGAGAGACAGA 724
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QY 725 TCACAGAGA 733
DB 1031 ACGCCAAGA 1039

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